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#29	Related Articles for PubMed (Select 11125283)	11:41:39	134
#27	Search TADG-15 or TADG15	11:39:43	4
#25	Search dickson[au] AND lin[au] AND (breast or T47* or T-47* or cancer or proteinase or protease)	11:30:24	21
#24	Search matriptase or TADG-15 or TADG15 or "membrane type serine protease-1" or "tumor antigen-derived gene 15 "	11:28:43	56
#23	Search matriptase or TADG-15 or TADG15 or "membrane type serine protease-1" or "tumor antigen-derived gene 15 " Field: Title/Abstract, Limits: Publication Date to 1999/03/12	11:28:11	0
#21	Search MTSP-1 or MTSP1 or matriptase or TADG-15 or TADG15 or "membrane type serine protease-1" or "tumor antigen-derived gene 15 " Field: Title/Abstract, Limits: Publication Date to 1999/03/12	11:26:59	14
#20	Search MTSP-1 or MTSP1 or matriptase or TADG-15 or TADG15 or "membrane type serine protease-1" or "tumor antigen-derived gene 15 " Field: Title/Abstract	11:26:41	62
#19	Search MTSP-1 or MTSP1 or matriptase or TADG-15 or TADG15 or "membrane type serine protease-1" or "tumor antigen-derived gene 15 "	11:26:32	70

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Jan 4 2005 07:12:41

57n

FILE 'HOME' ENTERED AT 11:59:12 ON 13 JAN 2005

L1 443 MTSP-1 OR MTSP1 OR MT-SP1 OR MATRIPTASE OR TADG-15 OR TADG15 OR
(MEMBRANE (A) TYPE OR MEMBRANE-TYPE) (A) SERINE (A) (PROTEASE-1
OR PROTEASE (A) 1) OR TUMOR (A) ANTIGEN-DERIVED (A) GENE (A) 15

L11 36 L3 AND (ANTIBOD? OR IMMUNOGLOB? OR IMMUNOASSAY OR MONOCLONAL
OR MAB)

(FILE 'HOME' ENTERED AT 11:59:12 ON 13 JAN 2005)

FILE 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH, LIFESCI, CANCERLIT'
ENTERED AT 12:00:10 ON 13 JAN 2005

L1 443 S MTSP-1 OR MTSP1 OR MT-SP1 OR MATRIPTASE OR TADG-15 OR TADG15
L2 282 S L1 AND (MT-SP1 OR MATRIPTASE OR TADG-15 OR TADG15)/AB
L3 163 DUP REM L1 (280 DUPLICATES REMOVED)
L4 88 S L3 AND L2
L5 6 S L4 AND PY<2000
L6 284 S L1 AND (CANCER OR TUMOR OR BREAST OR OVAR###)
L7 115 S L6 AND L3
L8 69 S L7 AND L2
L9 63 S L8 NOT L5
L10 10 S L7 AND PY<2000
L11 36 S L3 AND (ANTIBOD? OR IMMUNOGLOB? OR IMMUNOASSAY OR MONOCLONAL
L12 0 S L10 NOT L6
L13 4 S L10 NOT L5
L14 34 S L11 NOT (L10 OR L5)

L5 ANSWER 1 OF 6 MEDLINE on STN
 AN 1999432178 MEDLINE
 DN PubMed ID: 10500122
 TI Reverse biochemistry: use of macromolecular protease inhibitors to dissect complex biological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.
 AU Takeuchi T; Shuman M A; Craik C S
 CS Department of Pharmaceutical Chemistry, University of California, San Francisco, CA 94143, USA.
 NC CA71097 (NCI)
 CA72006 (NCI)
 SO Proceedings of the National Academy of Sciences of the United States of America, (1999 Sep 28) 96 (20) 11054-61.
 Journal code: 7505876. ISSN: 0027-8424.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 OS GENBANK-AF133086
 EM 199910
 ED Entered STN: 19991101
 Last Updated on STN: 20000303
 Entered Medline: 19991021
 AB Serine proteases of the chymotrypsin fold are of great interest because they provide detailed understanding of their enzymatic properties and their proposed role in a number of physiological and pathological processes. We have been developing the macromolecular inhibitor ecotin to be a "fold-specific" inhibitor that is selective for members of the chymotrypsin-fold class of proteases. Inhibition of protease activity through the use of wild-type and engineered ecotins results in inhibition of rat prostate differentiation and retardation of the growth of human PC-3 prostatic cancer tumors. In an effort to identify the proteases that may be involved in these processes, reverse transcription-PCR with PC-3 poly(A)+ mRNA was performed by using degenerate oligonucleotide primers. These primers were designed by using conserved protein sequences unique to chymotrypsin-fold serine proteases. Five proteases were identified: urokinase-type plasminogen activator, factor XII, protein C, trypsinogen IV, and a protease that we refer to as **membrane-type serine protease 1 (MT-SP1)**. The cloning and characterization of the **MT-SP1** cDNA shows that it encodes a mosaic protein that contains a transmembrane signal anchor, two CUB domains, four LDLR repeats, and a serine protease domain. Northern blotting shows broad expression of **MT-SP1** in a variety of epithelial tissues with high levels of expression in the human gastrointestinal tract and the prostate. A His-tagged fusion of the **MT-SP1** protease domain was expressed in Escherichia coli, purified, and autoactivated. Ecotin and variant ecotins are subnanomolar inhibitors of the **MT-SP1** activated protease domain, suggesting a possible role for **MT-SP1** in prostate differentiation and the growth of prostatic carcinomas.

L5 ANSWER 2 OF 6 MEDLINE on STN
 AN 1999303582 MEDLINE
 DN PubMed ID: 10373425
 TI Purification and characterization of a complex containing **matritptase** and a Kunitz-type serine protease inhibitor from human milk.
 AU Lin C Y; Anders J; Johnson M; Dickson R B
 CS Lombardi Cancer Center, Georgetown University Medical Center, Washington,

D.C. 20007, USA.
 NC 1P50CA58158 (NCI)
 P30-CA51005 (NCI)
 P30-CA51008 (NCI)
 SO Journal of biological chemistry, (1999 Jun 25) 274 (26)
 18237-42.
 Journal code: 2985121R. ISSN: 0021-9258.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199907
 ED Entered STN: 19990727
 Last Updated on STN: 20000303
 Entered Medline: 19990715
 AB **Matriptase**, a trypsin-like serine protease with two potential regulatory modules (low density lipoprotein receptor and complement C1r/s domains), was initially purified from T-47D breast cancer cells. Given its plasma membrane localization, extracellular matrix-degrading activity, and expression by breast cancer cells, this protease may be involved in multiple aspects of breast tumor progression, including cancer invasion. In breast cancer cells, **matriptase** was detected mainly as an uncomplexed form; however, low levels of **matriptase** were detected in complexes. In striking contrast, only the complexed **matriptase** was detected in human milk. The complexed **matriptase** has now been purified. Amino acid sequences obtained from the **matriptase**-associated proteins reveal that they are fragments of a Kunitz-type serine protease inhibitor that was previously reported to be an inhibitor of the hepatocyte growth factor activator. In addition, **matriptase** and its complexes were detected in milk-derived, SV40 T-antigen-immortalized mammary luminal epithelial cell lines, but not in human foreskin fibroblasts or in HT-1080 fibrosarcoma cells. These results suggest that the milk-derived **matriptase** complexes are likely to be produced by the epithelial components of the lactating mammary gland in vivo and that the activity and function of **matriptase** may be differentially regulated by its cognate inhibitor, comparing breast cancer with the lactating mammary gland.
 LS ANSWER 3 OF 6 MEDLINE on STN
 AN 1999303581 MEDLINE
 DN PubMed ID: 10373424
 TI Molecular cloning of cDNA for **matriptase**, a matrix-degrading serine protease with trypsin-like activity.
 AU Lin C Y; Anders J; Johnson M; Sang Q A; Dickson R B
 CS Lombardi Cancer Center, Georgetown University Medical Center, Washington, D. C. 20007, USA.
 NC 1P50CA58158 (NCI)
 P30-CA51005 (NCI)
 P30-CA51008 (NCI)
 SO Journal of biological chemistry, (1999 Jun 25) 274 (26) 18231-6.
 Journal code: 2985121R. ISSN: 0021-9258.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 OS GENBANK-AF118224
 EM 199907
 ED Entered STN: 19990727
 Last Updated on STN: 20000303
 Entered Medline: 19990715
 AB A major protease from human breast cancer cells was previously detected by

gelatin zymography and proposed to play a role in breast cancer invasion and metastasis. To structurally characterize the enzyme, we isolated a cDNA encoding the protease. Analysis of the cDNA reveals three sequence motifs: a carboxyl-terminal region with similarity to the trypsin-like serine proteases, four tandem cysteine-rich repeats homologous to the low density lipoprotein receptor, and two copies of tandem repeats originally found in the complement subcomponents C1r and C1s. By comparison with other serine proteases, the active-site triad was identified as His-484, Asp-539, and Ser-633. The protease contains a characteristic Arg-Val-Val-Gly-Gly motif that may serve as a proteolytic activation site. The bottom of the substrate specificity pocket was identified to be Asp-627 by comparison with other trypsin-like serine proteases. In addition, this protease exhibits trypsin-like activity as defined by cleavage of synthetic substrates with Arg or Lys as the P1 site. Thus, the protease is a mosaic protein with broad spectrum cleavage activity and two potential regulatory modules. Given its ability to degrade extracellular matrix and its trypsin-like activity, the name **matriptase** is proposed for the protease.

L5 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN

AN 1999:617620 CAPLUS

TI Structural basis of the interaction between **matriptase** and its cognate Kunitz-type inhibitor.

AU Lin, Chen-Yong; Enyedy, Istvan J.; Wang, Shaomeng; Dickson, Robert D.

CS Lombardi Cancer Center, Georgetown University, Washington, DC, 20007, USA

SO Book of Abstracts, 218th ACS National Meeting, New Orleans, Aug. 22-26 (1999), MEDI-246 Publisher: American Chemical Society, Washington, D. C.

CODEN: 67ZJAS

DT Conference; Meeting Abstract

LA English

AB **Matriptase** (MTP) is a trypsin-like serine protease proposed to play a role in breast cancer invasion and metastasis. MTP is found in human milk as a complex with a Kunitz-type inhibitor (KSPI), while in human breast cancer cells MTP and KSPI are mainly in uncomplexed form. Non-reduced/reduced diagonal gel electrophoresis of the uncomplexed and complexed MTP revealed that the complexed MTP is a two-chain protease; in contrast, the uncomplexed MTP is a single-chain protease. The cleavage site was identified to be the Arg residue that is located in the conserved activation motif (Arg-Val-Val-Gly-Gly). These results suggest that conversion of the single-chain MTP to two-chain MTP is required for the interaction between MTP and the KSPI. Computer modeling revealed that the KSPI Kunitz domain I, but not domain II is the functionally inhibitory domain that interacts with MTP. This is consistent with the observation that the 40-kDa fragment of the KSPI that exhibits binding affinity to MTP contains the Kunitz domain I, but does not contain the intact Kunitz domain II. Thus, the serine protease domain in active configuration of MTP and the Kunitz domain I of the KSPI are required for their interaction.

L5 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN

AN 1999:549168 CAPLUS

DN 131:181664

TI **TADG-15**: an extracellular serine protease overexpressed in breast and ovarian carcinomas

IN O'Brien, Timothy J.; Tanimoto, Hirotooshi

PA The Board of Trustees of the University of Arkansas, USA

SO PCT Int. Appl., 71 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 35

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9942120	A1	19990826	WO 1999-US3436	19990218 <--
	W: AU, CA, JP				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 5972616	A	19991026	US 1998-27337	19980220 <--
	CA 2324993	AA	19990826	CA 1999-2324993	19990218 <--
	AU 9928692	A1	19990906	AU 1999-28692	19990218 <--
	AU 750932	B2	20020801		
	EP 1056466	A1	20001206	EP 1999-909502	19990218
	EP 1056466	B1	20040121		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	AT 258060	E	20040215	AT 1999-909502	19990218
	PT 1056466	T	20040630	PT 1999-909502	19990218
	ES 2215376	T3	20041001	ES 1999-909502	19990218
	US 6649741	B1	20031118	US 2000-654600	20000901
	US 2004086910	A1	20040506	US 2003-600187	20030620
PRAI	US 1998-27337	A	19980220		
	WO 1999-US3436	W	19990218		
	US 1999-421213	A3	19991020		
	US 2000-654600	A3	20000901		

AB The invention provides a cDNA encoding a novel human extracellular serine protease termed **Tumor Antigen Derived Gene-15 (TADG-15)**. The cDNA sequence as well as the corresponding deduced amino acid sequence of human **TADG-15** are disclosed. Also disclosed is a vector capable of expressing the human **TADG-15** when transfected into a foreign host cell. In addition, a method (nucleic acid hybridization) for detecting the level of TADG-14 gene mRNA is disclosed. The **TADG-15** serine protease has been found to be overexpressed in breast and ovarian carcinomas. PCR primers specific for the **TADG-15** gene were constructed and used to show expression of **TADG-15** mRNA in ovarian carcinomas. Due to the extracellular nature of the **TADG-15** serine protease, it may be possible to exploit its expression as a diagnostic tool for ovarian cancer.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L5 ANSWER 6 OF 6 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN
AN 2000:294636 BIOSIS
DN PREV200000294636
TI **TADG-15**: an extracellular serine protease overexpressed in breast and ovarian carcinomas.
AU O'Brien, Timothy J. [Inventor, Reprint author]; Tanimoto, Hirotoshi [Inventor]
CS Little Rock, AR, USA
ASSIGNEE: The Board of Trustees of the University of Arkansas, Little Rock, AR, USA
PI US 5972616 October 26, 1999
SO Official Gazette of the United States Patent and Trademark Office Patents, (Oct. 26, 1999) Vol. 1227, No. 4. e-file.
CODEN: OGUPE7. ISSN: 0098-1133.
DT Patent
LA English
ED Entered STN: 6 Jul 2000
Last Updated on STN: 7 Jan 2002
AB The present invention provides a DNA encoding a **TADG-15**

protein selected from the group consisting of: (a) isolated DNA which encodes a **TADG-15** protein; (b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a **TADG-15** protein; and (c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a **TADG-15** protein. Also provided is a vector capable of expressing the DNA of the present invention adapted for expression in a recombinant cell and regulatory elements necessary for expression of the DNA in the cell.

L13 ANSWER 1 OF 4 MEDLINE on STN
 AN 94080664 MEDLINE
 DN PubMed ID: 8258142
 TI An ovalbumin peptide-specific cytotoxic T cell clone with antigen self-presentation capacity uses two distinct mechanisms to kill target cells.
 AU Dick T; Reichmann G; Ebnet K; Simon M M; Dienes H P; Echternacher B; Krammer P H; Reske-Kunz A B
 CS Institut fur Immunologie, Johannes Gutenberg Universitat, Mainz, Germany.
 SO Cellular immunology, (1993 Dec) 152 (2) 333-47.
 Journal code: 1246405. ISSN: 0008-8749.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199401
 ED Entered STN: 19940203
 Last Updated on STN: 20000303
 Entered Medline: 19940114
 AB Cloned 10BK.1 T cells with specificity for the ovalbumin peptide OVA257-264 are representative of a novel cell type within the CD8+ subset of T cells. In the presence and in the absence of added antigen presenting cells these T cells react toward antigen (Ag) by proliferation and lymphokine production. These data suggest self-presentation of the Ag by 10BK.1 cells. Here we present evidence that 10BK.1 cells exhibit cytotoxic activity that involves two different cytotoxic effector mechanisms. (i) One mechanism is fast killing activity, apparent within 4 hr. Constitutive mouse T cell-specific proteinase-1 (**MTSP-1**) activity, constitutive expression of **MTSP-1** RNA, increased by Ag challenge, and Ag-inducible perforin RNA expression were observed. Electron microscopic dense granules of the CTL were oriented toward Ag-pulsed target cells. The fast form of cytotoxicity was triggered by Ag recognition and by contact with IL-2. (ii) The other mechanism is slow cytolytic activity, manifested within 2 days. This activity was contained in the supernatant of 10BK.1 cells after Ag activation. It was inhibited by monoclonal anti-TNF antibodies and therefore presumably represents TNF alpha/beta. Cytotoxic T cells capable of antigen self-presentation may be responsible for tissue damage during bacterial and viral infections.

L13 ANSWER 2 OF 4 MEDLINE on STN
 AN 92223391 MEDLINE
 DN PubMed ID: 1562736
 TI A T-cell-related proteinase expressed by T-lymphoma cells activates their endogenous pro-urokinase.
 AU Brunner G; Vettel U; Jobstmann S; Kramer M D; Schirrmacher V
 CS German Cancer Research Center, Institute of Immunology and Genetics, Heidelberg.
 SO Blood, (1992 Apr 15) 79 (8) 2099-106.
 Journal code: 7603509. ISSN: 0006-4971.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Abridged Index Medicus Journals; Priority Journals
 EM 199205
 ED Entered STN: 19920607
 Last Updated on STN: 20000303
 Entered Medline: 19920515
 AB In this report, we investigated the expression and activation of proteolytic enzymes by mouse T-lymphoma cell lines of differing metastatic

potential. In contrast to the low metastatic Eb line, the metastatic variants ESb and ESb-MP secreted urokinase-type plasminogen activator (u-PA), which was present in the culture supernatant predominantly in the active form (ESb, 96%; ESb-MP, 80%). All three T-lymphoma variants expressed a mainly cell surface-associated proteinase, which proved to be immunologically and enzymatically related to the murine T-cell-associated serine proteinase-1 (**MTSP-1**). Intact lymphoma cells were able to activate the recombinant human proenzyme of u-PA (pro-u-PA) by a plasmin-independent mechanism, because plasmin contamination of the cells was not detectable. When ESb-MP cells were cultured in the presence of inhibitors of **MTSP-1**, such as antithrombin III, Pro-Phe-Arg-chloromethylketone, or aprotinin, the ratio of endogenously activated murine u-PA to inactive pro-u-PA in conditioned medium was significantly reduced (from 80% to 15%). The most potent inhibitor, antithrombin, did not inhibit plasmin-catalyzed pro-u-PA activation. These results suggest a novel autocrine mechanism of plasmin-independent pro-u-PA activation for metastatic T lymphomas by the production of an **MTSP-1**-related proteinase. The ability to initiate the proteolytic cascade of plasminogen activation in the absence of plasmin might contribute to the metastatic behavior of these cells observed in vivo.

L13 ANSWER 3 OF 4 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN
 AN 1999:97562 BIOSIS
 DN PREV199900097562
 TI Cloning and expression of **TADG-15**, a novel serine
 protease expressed in **ovarian cancer**.
 AU O'Brien, T. J.; Underwood, L. J.; Tanimoto, H.
 CS Univ. Arkansas Med. Sci., Little Rock, AR 72205, USA
 SO Tumor Biology, (Aug., 1998) Vol. 19, No. SUPPL. 2, pp. 33. print.
 Meeting Info.: 26th Meeting of the International Society for
 Oncodevelopmental Biology and Medicine. Umea, Sweden. August 30-September
 4, 1998.
 ISSN: 1010-4283.
 DT Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)
 LA English
 ED Entered STN: 4 Mar 1999
 Last Updated on STN: 4 Mar 1999

L13 ANSWER 4 OF 4 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation. on STN
 AN 1998:198282 BIOSIS
 DN PREV199800198282
 TI Cloning and expression of **TADG-15**, a novel serine
 protease expressed in **ovarian cancer**.
 AU Tanimoto, H.; Underwood, L. J.; Clarke, Y.; O'Brien, T. J.
 CS Univ. Arkansas Med. Sci., Little Rock, AR 72205, USA
 SO Proceedings of the American Association for Cancer Research Annual
 Meeting, (March, 1998) Vol. 39, pp. 648. print.
 Meeting Info.: 89th Annual Meeting of the American Association for Cancer
 Research. New Orleans, Louisiana, USA. March 28-April 1, 1998. American
 Association for Cancer Research.
 ISSN: 0197-016X.
 DT Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)
 LA English
 ED Entered STN: 4 May 1998
 Last Updated on STN: 4 May 1998

L14 ANSWER 6 OF 34 MEDLINE on STN
AN 2003042346 MEDLINE
DN PubMed ID: 12549907
TI Potent and selective inhibition of **membrane-type serine protease 1** by human single-chain **antibodies**.
AU Sun Jeonghoon; Pons Jaume; Craik Charles S
CS Department of Pharmaceutical Chemistry, University of California, San Francisco, 513 Parnassus, San Francisco, California 94143, USA.
NC CA72006 (NCI)
SO Biochemistry, (2003 Feb 4) 42 (4) 892-900.
Journal code: 0370623. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200303
ED Entered STN: 20030129
Last Updated on STN: 20030328
Entered Medline: 20030327
AB Specific human **antibodies** targeting proteases expressed on cancer cells can be valuable reagents for diagnosis, prognosis, and therapy of cancer. To this end, a phage-displayed **antibody** library was screened against a cancer-associated serine protease, **MT-SP1**. A protein inhibitor of serine proteases that binds to a defined surface of **MT-SP1** was used in an affinity-based washing procedure. Six **antibodies** were selected on the basis of their ELISA profiles and ability to serve as useful immunological reagents. The apparent $K(i)$, indicative of the potency of the **antibodies** at inhibiting human **MT-SP1** activity, ranged from 50 pM to 129 nM. Two of the **antibodies** had approximately 800-fold and 1500-fold selectivity when tested against the most homologous serine protease family member, mouse **MT-SP1**, that exhibits 86.6% sequence identity. Surface plasmon resonance was used as an independent means of determining the binding constants of the six **antibodies**. Association rates were as high as 1.15×10^7 s⁻¹ M⁻¹, and dissociation rates were as low as 3.8×10^{-4} s⁻¹. One **antibody** was shown to detect denatured **MT-SP1** with no cross reactivity to other family members in HeLa or PC3 cells. Another **antibody** recognized the enzyme in human prostate tissue samples for immunohistochemistry analysis. The mode of binding among the six **antibodies** and the protease was analyzed by competition ELISA using three distinctly different inhibitors that mapped the enzyme surface. These **antibodies** constitute a new class of highly selective protease inhibitors that can be used to dissect the biological roles of proteolytic enzymes as well as to develop diagnostic and therapeutic reagents.

L14 ANSWER 20 OF 34 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2003:717502 CAPLUS
DN 139:242266
TI **Immunoassay** for activated **matriptase** and its use in cancer diagnosis and treatment
IN Dickson, Robert B.; Lin, Chen-Yong; Benaud, Christelle; Oberst, Michael
PA USA
SO U.S. Pat. Appl. Publ., 41 pp.
CODEN: USXXCO
DT Patent
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2003170245	A1	20030911	US 2002-87987	20020305
PRAI	US 2002-87987		20020305		

AB The present invention provides an in vitro method of diagnosing the presence of a pre-malignant lesion, a malignancy, or other pathol. condition, in a subject, which is characterized by the presence of activated **matriptase** including the steps of: (A) obtaining a biol. sample from a subject that is to be tested for a pre-malignant lesion, a malignancy, or other pathol. condition; (B) exposing the biol. sample to a detectable agent which recognizes and binds to activated **matriptase**; and (C) determining whether said detectable agent is bound to the biol. sample. Preferably, the detectable agent is an **antibody** which specifically binds to activated **matriptase**. More preferably the **antibody** is selected from M69 and M123. The invention also provides a method of treating malignancies, pre-malignant conditions, and pathol. conditions in a subject which are characterized by the activated form of **matriptase** including administering a therapeutically effective amount of an agent capable of blocking the activity of active **matriptase**.

L14 ANSWER 25 OF 34 CAPLUS COPYRIGHT 2005 ACS on STN

AN 2002:90199 CAPLUS

DN 136:146188

TI Sequences of human **matriptase**-like serine protease and diagnostic and therapeutic uses thereof

IN Xiao, Yonghong

PA Bayer Aktiengesellschaft, Germany

SO PCT Int. Appl., 140 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002008392	A2	20020131	WO 2001-EP8182	20010716
	WO 2002008392	A3	20021121		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 2000-220807P P 20000725

US 2001-280109P P 20010402

AB Reagents which regulate human **matriptase**-like serine protease activity and reagents which bind to human **matriptase**-like serine protease gene products can be used to regulate extracellular matrix degradation. Such regulation is particularly useful for treating cancer, including metastasis of malignant cells, chronic obstructive pulmonary disease, disorders of the peripheral or central nervous system, and cardiovascular disorders.

L14 ANSWER 26 OF 34 CAPLUS COPYRIGHT 2005 ACS on STN

AN 2001:935392 CAPLUS

DN 136:64107

TI Structure-based discovery of inhibitors of **matriptase** for the

treatment of cancer and other conditions, and diagnostic methods
IN Lin, Chen-Yong; Dickson, Robert B.; Wang, Shaomeng; Enyedy, Istvan; Lee,
Sheau-Ling

PA Georgetown University, USA

SO PCT Int. Appl., 53 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001097794	A2	20011227	WO 2001-US18773	20010612
	WO 2001097794	A3	20030821		
	WO 2001097794	C1	20031030		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	EP 1355637	A2	20031029	EP 2001-944426	20010612
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
	US 2003092752	A1	20030515	US 2001-885295	20010621
	US 6677377	B2	20040113		
PRAI	US 2000-213073P	P	20000621		
	WO 2001-US18773	W	20010612		

OS MARPAT 136:64107

AB A method is provided for inhibiting carcinoma progression in which **matriptase** plays a role in a subject in need of such inhibition. The method includes administering to a subject an effective amount of a compound comprising two pos. charged groups, which are the same or different. The groups are linked by a chemical group having a length of 5-30 A, and preferably 15-24 A. Diagnostic methods based on **matriptase** action and therapeutic methods involving inhibition of **matriptase** activity are provided.

L14 ANSWER 27 OF 34 CAPLUS COPYRIGHT 2005 ACS on STN

AN 2001:380438 CAPLUS

DN 135:24657

TI Selective cellular targeting: multifunctional delivery vehicles

IN Glazier, Arnold

PA Drug Innovation & Design, Inc., USA

SO PCT Int. Appl., 981 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001036003	A2	20010525	WO 2000-US31262	20001114
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

CA 2391534 AA 20010525 CA 2000-2391534 20001114
 AU 2001016075 A5 20010530 AU 2001-16075 20001114
 EP 1255567 A1 20021113 EP 2000-978631 20001114

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

US 2003138432 A1 20030724 US 2000-738625 20001215
 PRAI US 1999-165485P P 19991115
 US 2000-239478P P 20001011
 US 2000-241937P P 20001020
 WO 2000-US31262 W 20001114
 US 2000-712465 B1 20001115

AB The present invention relates to the compns., methods, and applications of a novel approach to selective cellular targeting. The purpose of this invention is to enable the selective delivery and/or selective activation of effector mols. to target cells for diagnostic or therapeutic purposes. The present invention relates to multi-functional prodrugs or targeting vehicles wherein each functionality is capable of enhancing targeting selectivity, affinity, intracellular transport, activation or detoxification. The present invention also relates to ultralow dose, multiple target, multiple drug chemotherapy and targeted immunotherapy for cancer treatment.

L14 ANSWER 28 OF 34 CAPLUS COPYRIGHT 2005 ACS on STN

AN 2001:300733 CAPLUS

DN 134:322694

TI An extracellular serine protease **TADG-15** overexpressed in carcinomas and uses of **TADG-15** in diagnosis, treatment and prevention of cancer

IN O'brien, Timothy J.; Tanimoto, Hirotooshi

PA The Board of Trustees of the University of Arkansas, USA

SO PCT Int. Appl., 130 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 35

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001029056	A1	20010426	WO 2000-US29095	20001020
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 6649741	B1	20031118	US 2000-654600	20000901
	CA 2388450	AA	20010426	CA 2000-2388450	20001020
	EP 1226150	A1	20020731	EP 2000-973739	20001020
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
	JP 2003512036	T2	20030402	JP 2001-531854	20001020
	AU 774106	B2	20040617	AU 2001-12215	20001020
	US 2004086910	A1	20040506	US 2003-600187	20030620
PRAI	US 1999-421213	A	19991020		
	US 1998-27337	A2	19980220		
	US 2000-654600	A3	20000901		

WO 2000-US29095 W 20001020

AB The present invention provides cDNA encoding a **TADG-15** (**tumor antigen-derived gene 15**) serine protease from human that is overexpressed in ovarian tumors. **TADG-15** appears to be a transmembrane multidomain serine protease. The **TADG-15** cDNA is 3147 base pairs long encoding for a 855 amino acid protein. Also provided is a vector capable of expressing the DNA of the present invention adapted for expression in a recombinant cell and regulatory elements necessary for expression of the DNA in the cell. The present invention further provides for methods of inhibiting **TADG-15** expression and/or protease activity, methods of detecting **TADG-15** mRNA and/or protein and methods of screening for **TADG-15** inhibitors. Addnl., the present invention provides for cell-specific targeting via **TADG-15** and methods of vaccinating an individual against **TADG-15**. The methods described are useful in the diagnosis, treatment and prevention of cancer, particularly breast and ovarian cancer.

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 29 OF 34 CAPLUS COPYRIGHT 2005 ACS on STN

AN 2001:247459 CAPLUS

DN 134:294083

TI Characterization and diagnostic and therapeutic uses of cancer-associated **membrane type serine protease 1 (MT-SP1)**

IN Craik, Charles S.; Takeuchi, Toshihiko; Shuman, Marc

PA The Regents of the University of California, USA

SO PCT Int. Appl., 102 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001023524	A2	20010405	WO 2000-US27250	20001002
	W:			AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM	
	RW:			GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG	
	AU 2000079913	A5	20010430	AU 2000-79913	20001002
PRAI	US 1999-410362	A	19990930		
	WO 2000-US27250	W	20001002		

AB This invention provides cDNA and encoded amino acid sequences of a novel membrane-type serine protease (designated **MT-SP1**) elevated expression of which is associated with cancer. In one embodiment, this invention provides a method obtaining a prognosis or of detecting or staging a cancer in an organism. The method involves providing a biol. sample from the organism and detecting the level of a **membrane-type serine protease 1 (MT-SP1)** in the sample, where an elevated level of the membrane-type serine protease, as compared to the level of the protease in a biol. sample from a normal healthy organism indicates the presence or stage of the cancer.

L14 ANSWER 30 OF 34 CAPLUS COPYRIGHT 2005 ACS on STN

AN 2000:645893 CAPLUS

DN 133:234748

TI **Matriptase**, a serine protease and its applications in detection of breast or other cancers

IN Dickson, Robert B.; Lin, Chen-Yong; Johnson, Michael; Wang, Shaomeng; Enyedy, Istvan

PA Georgetown University, USA

SO PCT Int. Appl., 116 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000053232	A1	20000914	WO 2000-US6111	20000310
	W: CA, JP, US				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	CA 2362670	AA	20000914	CA 2000-2362670	20000310
	EP 1161266	A1	20011212	EP 2000-914875	20000310
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2002539093	T2	20021119	JP 2000-603721	20000310
PRAI	US 1999-124006P	P	19990312		
	WO 2000-US6111	W	20000310		

AB The invention is directed to a method of detecting a malignancy or a pre-malignant lesion in breast or other tissue, or a pathol. condition, by detecting the presence of single-chain or two-chain forms of **matriptase** in the tissue. The invention is further directed to a method of treating malignancies, which have the phenotype of **matriptase** production by administering a tumor formation inhibiting effective amount of a concentrate of Bowman-Birk inhibitor (BBIC), or other **matriptase** inhibitor. The invention also is directed to nucleic acids encoding a **matriptase** protein or fragments thereof, and their use for structure elucidation and modeling to identify other inhibitors of **matriptase**, as well as to methods of identifying **matriptase** modulating agents, including activators and inhibitors.

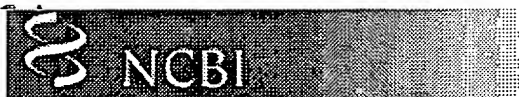
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

WEST Search History

DATE: Thursday, January 13, 2005

Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
		<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L11	L10 not (l6 or l7)	14
<input type="checkbox"/>	L10	L9 and (antibod\$ or immunoglob\$)	18
<input type="checkbox"/>	L9	(MTSP-1 or TADG15 or TADG-15 or Tumor adj Antigen adj derived adj Gene-15)	22
<input type="checkbox"/>	L8	(MTSP-1 or TADG15 or Tumor adj Antigen adj derived adj Gene-15)	10
<input type="checkbox"/>	L7	membrane adj type adj serine adj protease-1	3
<input type="checkbox"/>	L6	l5 and (antibod\$ or immunoglob\$ or immunoassay)	4
<input type="checkbox"/>	L5	(MTSP-1 or TADG15) same (breast or cancer or tumor or serine adj protease)	4
<input type="checkbox"/>	L4	L3 and l1	140
<input type="checkbox"/>	L3	(\$proteinase or \$protease) same (breast adj (tumor or cancer) or T47D\$)	706
<input type="checkbox"/>	L2	L1 and (80 adj (kDA or kilodalton) or 80-kda or 80kda or 80-kilo\$)	11
<input type="checkbox"/>	L1	(matriptase or serine adj protease same (milk\$ or breast\$))	307

END OF SEARCH HISTORY



results of BLAST

BLASTP 2.2.10 [Oct-19-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1105627453-27392-10571710208.BLASTQ4

Query=

(855 letters)

Database: All non-redundant GenBank CDS

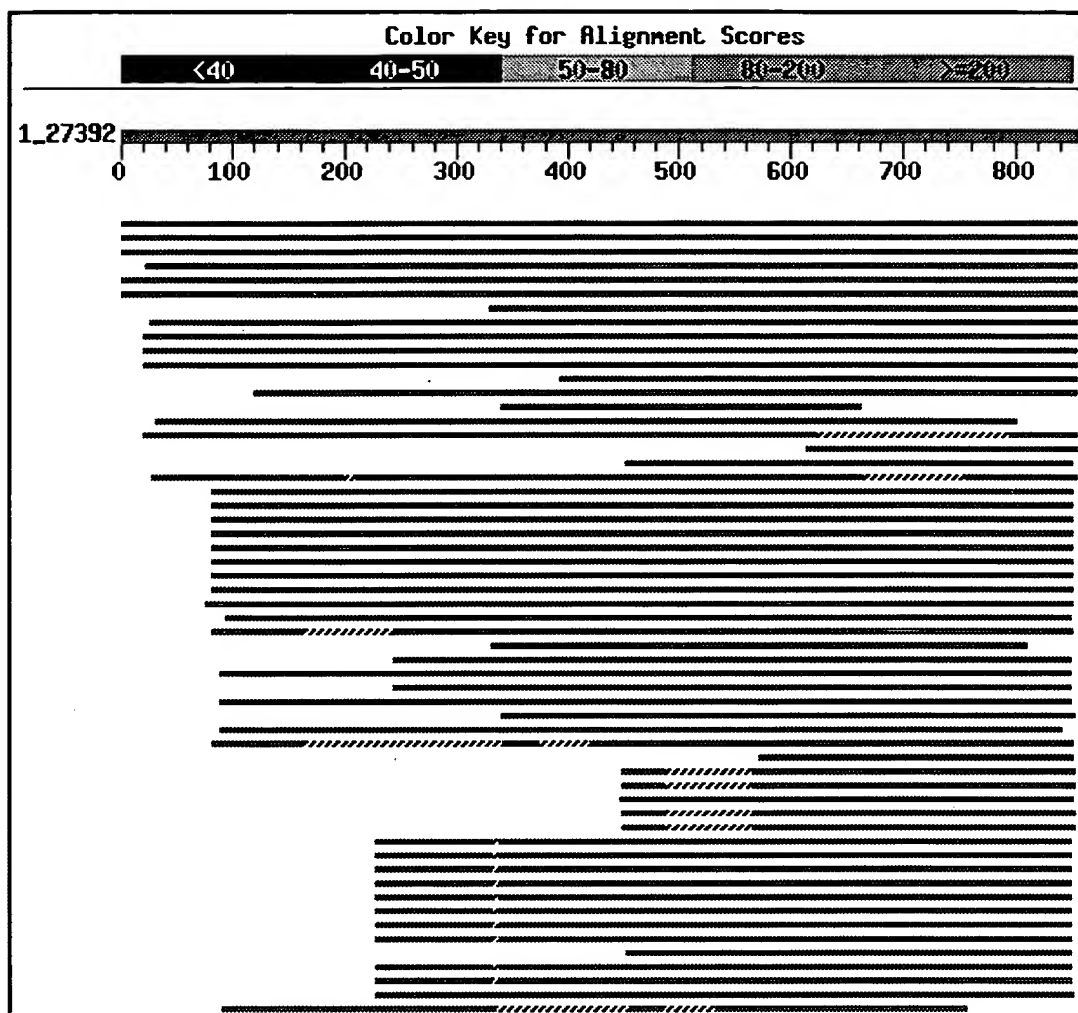
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
2,304,535 sequences; 784,226,776 total letters

If you have any problems or questions with the results of this search please refer to the **BLAST FAQs**

Taxonomy reports

Distribution of 655 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Related Structures

Sequences producing significant alignments:			Score (bits)	E Value	
gi 11415040 ref NP_068813.1 	matriptase [Homo sapiens]	>gi ...	1698	0.0	G
gi 12249015 dbj BAB20376.1 	prostamin [Homo sapiens]		1696	0.0	G
gi 10257390 gb AAG15395.1 	serine protease TADG15 [Homo sap...		1696	0.0	G
gi 55637345 ref XP_508863.1 	PREDICTED: similar to matripta...		1444	0.0	
gi 7363445 ref NP_035306.2 	suppression of tumorigenicity 1...		1438	0.0	G
gi 16758444 ref NP_446087.1 	suppression of tumorigenicity ...		1433	0.0	G
gi 34782939 gb AAH05826.2 	ST14 protein [Homo sapiens]		1145	0.0	G
gi 50760033 ref XP_417872.1 	PREDICTED: similar to suppress...		1095	0.0	G
gi 49257232 gb AAH71077.1 	St14-A-prov protein [Xenopus lae...		1008	0.0	G
gi 9757702 dbj BAB08218.1 	homolog of human MT-SP1 [Xenopus...		998	0.0	G
gi 52354617 gb AAH82854.1 	Unknown (protein for MGC:81690) ...		993	0.0	
gi 17390323 gb AAH18146.1 	ST14 protein [Homo sapiens]		920	0.0	G
gi 47225569 emb CAG12052.1 	unnamed protein product [Tetrao...		740	0.0	
gi 10179932 gb AAG13949.1 	serine protease SNC19 [Homo sapi...		727	0.0	G
gi 47227882 emb CAG09045.1 	unnamed protein product [Tetrao...		702	0.0	

gi 49900216 gb AAH76994.1 	MGC89623 protein [Xenopus tropic...	690	0.0	G
gi 18655574 pdb 1EAX A	Chain A, Crystal Structure Of Mtsp1 ...	512	e-143	S
gi 47209610 emb CAF89594.1 	unnamed protein product [Tetrao...	453	e-126	
gi 57086055 ref XP_546396.1 	PREDICTED: similar to matripta...	436	e-120	
gi 56417706 emb CAI19335.1 	OTTHUMP00000028798 [Homo sapiens]	398	e-109	
gi 34784418 gb AAH57674.1 	Tmprss6 protein [Mus musculus]	397	e-109	G
gi 31980537 gb AAP69827.1 	matriptase-2 [Mus musculus] >gi ...	397	e-109	G
gi 27229129 ref NP_082178.1 	type II transmembrane serine p...	395	e-108	G
gi 23957702 ref NP_705837.1 	transmembrane protease, serine...	393	e-107	G
gi 37181921 gb AAQ88764.1 	PVAE354 [Homo sapiens]	392	e-107	G
gi 23477115 emb CAC85953.1 	matriptase-2 [Homo sapiens]	392	e-107	G
gi 47678423 emb CAG30332.1 	dJ1170K4.2 [Homo sapiens]	380	e-103	G
gi 50728784 ref XP_416281.1 	PREDICTED: similar to PVAE354 ...	379	e-103	G
gi 51464094 ref XP_293599.5 	PREDICTED: transmembrane serin...	378	e-103	G
gi 57092775 ref XP_531743.1 	PREDICTED: similar to transmem...	371	e-101	
gi 47223349 emb CAG04210.1 	unnamed protein product [Tetrao...	371	e-101	
gi 33186804 tpe CAD67577.1 	TPA: type II transmembrane seri...	365	4e-99	G
gi 34869328 ref XP_221464.2 	similar to hypothetical protei...	364	5e-99	G
gi 27369619 ref NP_766043.1 	transmembrane serine protease ...	363	2e-98	G
gi 57109624 ref XP_545095.1 	PREDICTED: similar to type II ...	360	8e-98	
gi 50729728 ref XP_416635.1 	PREDICTED: similar to type II ...	350	1e-94	G
gi 55620796 ref XP_516646.1 	PREDICTED: similar to type II ...	319	2e-85	
gi 34866910 ref XP_235768.2 	similar to type II transmembra...	292	3e-77	G
gi 47217321 emb CAG12529.1 	unnamed protein product [Tetrao...	287	8e-76	
gi 55647901 ref XP_524042.1 	PREDICTED: similar to transmem...	279	2e-73	
gi 34862709 ref XP_234914.2 	similar to polyserase 1A prote...	277	8e-73	G
gi 33667063 ref NP_892018.1 	transmembrane serine protease ...	277	1e-72	G
gi 50760956 ref XP_425880.1 	PREDICTED: similar to transmem...	277	1e-72	G
gi 33341912 emb CAD35759.1 	polyserase-IB protein [Homo sap...	277	1e-72	G
gi 57102210 ref XP_542189.1 	PREDICTED: similar to transmem...	268	4e-70	
gi 47575834 ref NP_001001259.1 	enteropeptidase, light chai...	245	4e-63	G
gi 627699 pir A53663	enteropeptidase (EC 3.4.21.9) precurs...	245	4e-63	
gi 55656832 ref XP_514836.1 	PREDICTED: enterokinase [Pan t...	244	1e-62	
gi 55655639 ref XP_531395.1 	PREDICTED: enterokinase [Pan t...	244	1e-62	
gi 1589367 prf 2211228A	enteropeptidase	242	3e-62	
gi 27806097 ref NP_776864.1 	protease, serine, 7 [enterokin...	242	4e-62	G
gi 57108850 ref XP_544824.1 	PREDICTED: similar to enterope...	241	9e-62	
gi 4506151 ref NP_002763.1 	enterokinase precursor [Homo sa...	240	1e-61	G
gi 29244926 ref NP_006578.2 	corin [Homo sapiens]	237	1e-60	G
gi 4884872 gb AAD31850.1 	corin [Homo sapiens] >gi 13878447...	237	1e-60	G
gi 26332511 dbj BAC29973.1 	unnamed protein product [Mus mu...	236	2e-60	G
gi 7768763 dbj BAA95557.1 	enterokinase [Homo sapiens]	235	4e-60	
gi 57095842 ref XP_539291.1 	PREDICTED: similar to airway t...	233	2e-59	
gi 50729868 ref XP_425539.1 	PREDICTED: similar to enterope...	233	2e-59	G
gi 6679489 ref NP_032967.1 	protease, serine, 7 (enterokina...	232	4e-59	G
gi 57095850 ref XP_539295.1 	PREDICTED: similar to Serine p...	227	1e-57	
gi 34876793 ref XP_223301.2 	similar to hypothetical protei...	226	3e-57	G
gi 6648960 gb AAF21308.1 	mosaic serine protease epithelias...	225	5e-57	G
gi 37183152 gb AAQ89376.1 	serine protease [Homo sapiens] >...	224	7e-57	G

gi 6137097 qb AAF04328.1 	serine protease DESC1 [Homo sapiens]	224	7e-57	G
gi 34328226 ref NP_056590.2 	transmembrane protease, serine...	224	1e-56	G
gi 23512211 qb AAH38393.1 	Transmembrane protease, serine 2...	223	1e-56	G
gi 9739019 qb AAF97867.1 	serine protease TMPRSS2 [Mus musc...	223	2e-56	G
gi 51711154 ref XP_487870.1 	similar to airway trypsin-like...	222	4e-56	G
gi 40254733 ref NP_569108.2 	transmembrane protease, serine...	222	4e-56	G
gi 16444962 dbj BAB70683.1 	TMPRSS2 [Rattus norvegicus]	221	7e-56	G
gi 51571899 ref NP_001003979.1 	airway trypsin-like 3 [Ratt...	219	3e-55	G
gi 47550925 ref NP_999636.1 	cortical granule serine protea...	219	3e-55	G
gi 55622696 ref XP_517261.1 	PREDICTED: similar to DESC1 pr...	218	8e-55	
gi 29650889 qb AAO86772.1 	corin [Rattus norvegicus] >gi 32...	217	1e-54	G
gi 50729985 ref XP_416737.1 	PREDICTED: similar to transmem...	214	7e-54	G
gi 9757700 dbj BAB08217.1 	embryonic serine protease-2 [Xen...	214	9e-54	G
gi 8394057 ref NP_058565.1 	corin [Mus musculus] >gi 751371...	213	2e-53	G
gi 27370340 ref NP_766468.1 	type II transmembrane serine p...	212	3e-53	G
gi 55560104 qb AAV52922.1 	type II transmembrane serine pro...	212	3e-53	
gi 47077010 dbj BAD18439.1 	unnamed protein product [Homo s...	212	3e-53	
gi 46249844 qb AAH68636.1 	Unknown (protein for MGC:79882) ...	212	4e-53	
gi 6435698 pdb 1EKB B	Chain B, The Serine Protease Domain O...	211	7e-53	G S
gi 30089303 dbj BAC75886.1 	mannose-binding lectin associat...	211	7e-53	
gi 34859342 ref XP_215087.2 	similar to hypothetical protei...	209	3e-52	G
gi 50747079 ref XP_426340.1 	PREDICTED: similar to Atrial n...	208	6e-52	G
gi 50746867 ref XP_426319.1 	PREDICTED: similar to Serine p...	208	6e-52	G
gi 30089307 dbj BAC75888.1 	mannose-binding lectin associat...	208	6e-52	
gi 50843972 qb AAT84164.1 	enterokinase light chain [Bos ta...	207	1e-51	G
gi 17981042 qb AAL50817.1 	airway trypsin-like protease [Ra...	207	1e-51	G
gi 56270244 qb AAH86738.1 	Zgc:101791 [Danio rerio] >gi 566...	206	3e-51	
gi 34867472 ref XP_213668.2 	similar to enteropeptidase [Ra...	205	4e-51	G
gi 12018322 ref NP_072152.1 	adrenal secretory serine prote...	205	5e-51	G
gi 14091028 qb AAK53559.1 	epitheliasin [Homo sapiens]	204	9e-51	G
gi 2507613 qb AAC51784.1 	serine protease [Homo sapiens]	204	1e-50	G
gi 14602459 ref NP_005647.2 	transmembrane protease, serine...	203	2e-50	G
gi 30353995 qb AAH51839.1 	Transmembrane protease, serine 2...	202	3e-50	G
gi 51762028 ref XP_486010.1 	RIKEN cDNA C330007D15 [Mus mus...	202	3e-50	G
gi 57095844 ref XP_539292.1 	PREDICTED: similar to epiderma...	201	6e-50	
gi 21704106 ref NP_663536.1 	airway trypsin-like protease p...	200	2e-49	G
gi 33187750 qb AAP97729.1 	airway trypsin-like protease pre...	200	2e-49	G
gi 17864976 qb AAL47139.1 	airway trypsin-like protease [Mu...	200	2e-49	G
gi 47211451 emb CAG12258.1 	unnamed protein product [Tetrao...	199	3e-49	
gi 18141559 ref NP_542765.1 	transmembrane protease, serine...	198	5e-49	G
gi 28194548 qb AAO33581.1 	transmembrane proteinase serine ...	198	5e-49	
gi 22797097 emb CAD22137.1 	type II transmembrane serine pr...	198	7e-49	G
gi 52789219 qb AAH83024.1 	Unknown (protein for MGC:97879) ...	196	2e-48	
gi 47225057 emb CAF97472.1 	unnamed protein product [Tetrao...	196	2e-48	
gi 37182040 qb AAQ88823.1 	ECHOS1 [Homo sapiens] >gi 509606...	194	7e-48	G
gi 31238311 ref XP_319745.1 	ENSANGP00000006359 [Anopheles ...	194	7e-48	G
gi 54639460 qb EAL28862.1 	GA18102-PA [Drosophila pseudoobs...	194	9e-48	
gi 4758508 ref NP_004253.1 	airway trypsin-like protease [H...	194	1e-47	G

gi 24651942 ref NP_610436.1 	CG11824-PA [Drosophila melanog...	194	1e-47	G
gi 55622800 ref XP_526607.1 	PREDICTED: airway trypsin-like...	193	2e-47	
gi 46409446 ref NP_997290.1 	FLJ16046 protein [Homo sapiens...	193	2e-47	G
gi 54636457 gb EAL25860.1 	GA11219-PA [Drosophila pseudoobs...	193	2e-47	
gi 55235309 gb EAL39005.1 	ENSANGP00000028900 [Anopheles ga...	191	6e-47	
gi 13507652 ref NP_109634.1 	transmembrane protease, serine...	191	6e-47	G
gi 13878822 sp Q9ER04 TMS5 MOUSE	Transmembrane protease, se...	191	6e-47	G
gi 12248777 dbj BAB20276.1 	type 2 spinesin [Mus musculus]	191	6e-47	G
gi 12248781 dbj BAB20278.1 	type 1 spinesin [Mus musculus]	191	6e-47	G
gi 13959319 sp Q61129 CFAI MOUSE	Complement factor I precur...	191	6e-47	G
gi 57088547 ref XP_547177.1 	PREDICTED: similar to marapsin...	191	8e-47	
gi 51591911 ref NP_001004020.1 	airway trypsin-like 5 [Ratt...	191	1e-46	G
gi 34419641 ref NP_899234.1 	ovochymase 1 [Homo sapiens] >g...	191	1e-46	G
gi 26325646 dbj BAC26577.1 	unnamed protein product [Mus mu...	191	1e-46	G
gi 13173471 ref NP_076927.1 	transmembrane protease, serine...	190	2e-46	G
gi 1079140 pir A47547	serine proteinase stubble-stubbloid...	190	2e-46	
gi 17136448 ref NP_476709.1 	CG4316-PA [Drosophila melanoga...	190	2e-46	G
gi 55667225 ref XP_520817.1 	PREDICTED: similar to ovochyma...	190	2e-46	
gi 49481858 gb AAT66641.1 	transmembrane protease serine 3 ...	190	2e-46	
gi 23463311 ref NP_695223.1 	adrenal mitochondrial protease...	190	2e-46	G
gi 22770864 gb AAN06758.1 	adrenal mitochondrial protease s...	190	2e-46	G
gi 21429106 gb AAM50272.1 	LD44584p [Drosophila melanogaster]	190	2e-46	
gi 13162353 ref NP_077071.1 	complement factor I [Rattus no...	189	2e-46	G
gi 21669679 dbj BAC01864.1 	complement factor I [Triakis sc...	189	3e-46	
gi 33416784 gb AAH56000.1 	MGC68910 protein [Xenopus laevis]	189	4e-46	G
gi 49522964 gb AAH75293.1 	Transmembrane serine protease 9 ...	189	4e-46	G
gi 20072342 gb AAH26555.1 	Kallikrein B, plasma 1 [Mus musc...	189	4e-46	G
gi 32189423 ref NP_848845.1 	RIKEN cDNA 4732406D01 gene [Mu...	188	5e-46	G
gi 13540535 ref NP_110397.1 	transmembrane protease, serine...	188	5e-46	G
gi 48130453 ref XP_393317.1 	similar to ENSANGP00000006359 ...	188	5e-46	G
gi 26331844 dbj BAC29652.1 	unnamed protein product [Mus mu...	188	7e-46	G
gi 57095848 ref XP_539294.1 	PREDICTED: similar to RIKEN cD...	188	7e-46	
gi 6680267 ref NP_032307.1 	hepsin [Mus musculus] >gi 26060...	188	7e-46	G
gi 28892897 ref NP_795998.1 	RIKEN cDNA 9930019B18 gene [Mu...	188	7e-46	G
gi 30179800 sp O35453 HEPS MOUSE	Serine protease hepsin	188	7e-46	G
gi 27695202 gb AAH41753.1 	MGC53615 protein [Xenopus laevis]	187	9e-46	G
gi 47228191 emb CAG07586.1 	unnamed protein product [Tetrao...	187	9e-46	
gi 6680584 ref NP_032481.1 	kallikrein B, plasma 1 [Mus mus...	187	1e-45	G
gi 55728266 emb CAH90878.1 	hypothetical protein [Pongo pyg...	187	1e-45	
gi 21312500 ref NP_082342.1 	coagulation factor XI [Mus mus...	187	2e-45	G
gi 50746923 ref XP_420678.1 	PREDICTED: similar to Coagulat...	187	2e-45	G
gi 6009515 dbj BAA84941.1 	epidermis specific serine protea...	187	2e-45	G
gi 45708911 gb AAH67937.1 	Hypothetical protein MGC69547 [X...	186	2e-45	G
gi 50603930 gb AAH77417.1 	Klkb1-prov protein [Xenopus laevis]	186	3e-45	G
gi 14042984 ref NP_114435.1 	mosaic serine protease [Homo s...	186	3e-45	G
gi 13429970 dbj BAB39741.1 	membrane-type mosaic serine pro...	186	3e-45	G
gi 55391473 gb AAH85323.1 	Unknown (protein for MGC:103261)...	186	3e-45	
gi 38089812 ref XP_150167.3 	similar to BC010843 protein [M...	186	3e-45	G

gi 27503083 gb AAH42878.1 	BC010843 protein [Mus musculus]	186	3e-45	
gi 34877566 ref XP_343616.1 	similar to polyserase 1A prote...	185	4e-45	
gi 28893147 ref NP_796136.1 	RIKEN cDNA 9930032022 gene [Mu...	185	4e-45	
gi 55732638 emb CAH93018.1 	hypothetical protein [Pongo pyg...	185	4e-45	
gi 13811665 gb AAK40233.1 	coagulation factor XI [Mus muscu...	185	4e-45	
gi 26331892 dbj BAC29676.1 	unnamed protein product [Mus mu...	185	4e-45	
gi 33695155 ref NP_892028.1 	hepsin (transmembrane protease...	185	6e-45	
gi 34864591 ref XP_236201.2 	similar to mosaic serine prote...	185	6e-45	
gi 57038394 ref XP_541697.1 	PREDICTED: similar to Serine p...	185	6e-45	
gi 899286 emb CAA30058.1 	hepsin [Homo sapiens]	185	6e-45	
gi 57095846 ref XP_539293.1 	PREDICTED: similar to FLJ16046...	184	7e-45	
gi 47575881 ref NP_891994.2 	marapsin [Rattus norvegicus] >...	184	7e-45	
gi 28371868 gb AAO38062.1 	transmembrane protease serine 6 ...	184	7e-45	
gi 49354669 gb AAT65076.1 	mannan-binding lectin-associated...	184	7e-45	
gi 45861650 gb AAS78642.1 	epidermal type II transmembrane ...	184	7e-45	
gi 47223348 emb CAG04209.1 	unnamed protein product [Tetrao...	184	7e-45	
gi 2144494 pir PLPG	plasmin (EC 3.4.21.7) precursor - pig ...	184	1e-44	
gi 47271483 ref NP_872412.2 	hypothetical protein LOC339967...	184	1e-44	
gi 33438175 dbj BAC81507.1 	marapsin [Rattus norvegicus]	184	1e-44	
gi 6981134 ref NP_036857.1 	kallikrein B, plasma 1 [Rattus ...	184	1e-44	
gi 14602455 ref NP_115780.1 	transmembrane protease, serine...	184	1e-44	
gi 33186820 tpe CAD67985.1 	TPA: airway trypsin-like protea...	184	1e-44	
gi 34852404 ref XP_228059.2 	similar to type II transmembra...	183	2e-44	
gi 31222386 ref XP_317171.1 	ENSANGP00000006721 [Anopheles ...	183	2e-44	
gi 55643231 ref XP_510751.1 	PREDICTED: similar to marapsin...	183	2e-44	
gi 55726525 emb CAH90030.1 	hypothetical protein [Pongo pyg...	183	2e-44	
gi 4506153 ref NP_002764.1 	prostasin preproprotein [Homo s...	183	2e-44	
gi 31206367 ref XP_312135.1 	ENSANGP000000022018 [Anopheles ...	183	2e-44	
gi 55622798 ref XP_526606.1 	PREDICTED: similar to epiderma...	183	2e-44	
gi 56550205 emb CAE84572.1 	DESC4 protein [Rattus norvegicus]	183	2e-44	
gi 7512178 pir T30337	polyprotein - African clawed frog >g...	182	5e-44	
gi 8393560 ref NP_058808.1 	hepsin [Rattus norvegicus] >gi ...	181	6e-44	
gi 57087877 ref XP_547044.1 	PREDICTED: hypothetical protei...	181	6e-44	
gi 55623100 ref XP_526653.1 	PREDICTED: I factor (complemen...	181	6e-44	
gi 37183329 gb AAQ89464.1 	MPN [Homo sapiens] >gi 13994276 ...	181	8e-44	
gi 57109206 ref XP_535694.1 	PREDICTED: similar to Compleme...	181	8e-44	
gi 56676362 ref NP_001008554.1 	serine protease Desc4 [Ratt...	181	8e-44	
gi 20301968 ref NP_620191.1 	protease, serine, 8 (prostasin...	181	8e-44	
gi 38197638 gb AAH61800.1 	Protease, serine, 8 (prostasin) ...	181	8e-44	
gi 47228305 emb CAG07700.1 	unnamed protein product [Tetrao...	181	8e-44	
gi 1806583 gb AAC48717.1 	plasminogen	181	8e-44	
gi 264603 gb AAB25192.1 	miniplasminogen, MOPG [sheep, Pept...	181	1e-43	
gi 31222378 ref XP_317170.1 	ENSANGP000000018367 [Anopheles ...	181	1e-43	
gi 55241989 gb EAA07896.2 	ENSANGP000000022018 [Anopheles ga...	181	1e-43	
gi 50730061 ref XP_425558.1 	PREDICTED: similar to ECHOS1 [...	181	1e-43	
gi 2118101 pir B61545	plasmin (EC 3.4.21.7) precursor - sh...	181	1e-43	
gi 56199562 gb AAV84270.1 	serine protease [Culicoides sono...	180	1e-43	
gi 55237398 gb EAA12590.3 	ENSANGP000000018367 [Anopheles ga...	180	1e-43	
gi 27817290 emb CAD61105.1 	SI:dZ69G10.3 (novel protein sim...	180	1e-43	
gi 410328 emb CAA80517.1 	trypsin [Anopheles gambiae] >gi 6...	180	1e-43	
gi 55669526 pdb 1O5F H	Chain H, Dissecting And Designing In...	180	2e-43	

gi 47225686 emb CAG08029.1 	unnamed protein product [Tetrao...	180	2e-43	
gi 47522962 ref NP_999239.1 	kallikrein [Sus scrofa] >gi 41...	179	2e-43	
gi 2599504 qb AAB96905.1 	serine protease [Xenopus laevis]	179	2e-43	
gi 4504877 ref NP_000883.1 	plasma kallikrein B1 precursor ...	179	3e-43	
gi 31222400 ref XP_317173.1 	ENSANGP00000018384 [Anopheles ...	179	3e-43	
gi 55237402 qb EAA12264.2 	ENSANGP00000018384 [Anopheles ga...	179	3e-43	
gi 20142083 dbj BAB88921.1 	complement control protein fact...	179	4e-43	
gi 42543248 pdb 1P57 B	Chain B, Extracellular Domain Of Hum...	179	4e-43	
gi 116133 sp P05156 CFAI HUMAN	Complement factor I precursore...	178	5e-43	
gi 55623630 ref XP_526757.1 	PREDICTED: plasma kallikrein B...	178	5e-43	
gi 1335054 emb CAA68416.1 	unnamed protein product [Homo sa...	178	5e-43	
gi 55729915 emb CAH91684.1 	hypothetical protein [Pongo pyg...	178	5e-43	
gi 410326 emb CAA80515.1 	trypsin [Anopheles gambiae] >gi 6...	178	5e-43	
gi 50540258 ref NP_001002596.1 	zgc:92313 [Danio rerio] >gi...	178	7e-43	
gi 32698841 ref NP_872308.1 	hypothetical protein DKFZp686L...	177	9e-43	
gi 2331217 qb AAB66878.1 	trypsin [Anopheles stephensi]	177	9e-43	
gi 28202035 ref NP_780649.1 	pancreasin [Mus musculus] >gi ...	177	1e-42	
gi 47507258 qb AAH70996.1 	Unknown (protein for MGC:79928) ...	177	2e-42	
gi 410330 emb CAA80512.1 	trypsin [Anopheles gambiae] >gi 4...	176	2e-42	
gi 57097947 ref XP_532838.1 	PREDICTED: similar to Plasma k...	176	2e-42	
gi 41393105 ref NP_958880.1 	plasminogen [Danio rerio] >gi ...	176	2e-42	
gi 410327 emb CAA80516.1 	Trypsinogen precursor of ANTRYP7 ...	176	2e-42	
gi 25005112 qb AAN71006.1 	plasminogen precursor [Danio rerio]	176	2e-42	
gi 34980909 qb AAH57186.1 	Plg protein [Mus musculus] >gi 1...	176	3e-42	
gi 56199540 qb AAV84259.1 	serine protease [Culicoides sono...	176	3e-42	
gi 38051823 qb AAH60513.1 	Plasminogen [Homo sapiens]	176	3e-42	
gi 55732729 emb CAH93062.1 	hypothetical protein [Pongo pyg...	176	3e-42	
gi 55730120 emb CAH91784.1 	hypothetical protein [Pongo pyg...	176	3e-42	
gi 55727336 emb CAH90424.1 	hypothetical protein [Pongo pyg...	176	3e-42	
gi 9961353 ref NP_062505.1 	platelet coagulation factor XI ...	176	3e-42	
gi 6671744 ref NP_031712.1 	complement component factor i [...	176	3e-42	
gi 4503627 ref NP_000119.1 	platelet coagulation factor XI ...	176	3e-42	
gi 180352 qb AAA51985.1 	coagulation factor XI	176	3e-42	
gi 24657332 ref NP_652645.1 	CG18735-PA [Drosophila melanog...	176	3e-42	
gi 311983 emb CAA79327.1 	trypsin [Anopheles gambiae] >gi 4...	175	5e-42	
gi 2144495 pir PLMS	plasmin (EC 3.4.21.7) precursor - mous...	175	5e-42	
gi 31222393 ref XP_317172.1 	ENSANGP00000018316 [Anopheles ...	175	5e-42	
gi 55237401 qb EAA12262.3 	ENSANGP00000018316 [Anopheles ga...	175	5e-42	
gi 19032293 dbj BAB85634.1 	trypsinogen [Anguilla japonica]	175	6e-42	
gi 2815618 qb AAB97887.1 	plasminogen [Papio hamadryas]	175	6e-42	
gi 190026 qb AAA36451.1 	plasminogen	175	6e-42	
gi 37362124 qb AAQ91197.1 	prostasin [Mus musculus] >gi 191...	174	8e-42	
gi 387031 qb AAA60124.1 	plasminogen	174	8e-42	
gi 625234 pir PLHU	plasmin (EC 3.4.21.7) precursor [valida...	174	8e-42	
gi 4505881 ref NP_000292.1 	plasminogen [Homo sapiens] >gi ...	174	8e-42	
gi 31209815 ref XP_313874.1 	ENSANGP00000011601 [Anopheles ...	174	8e-42	
gi 6137624 pdb 1BUI B	Chain B, Structure Of The Ternary Mic...	174	8e-42	
gi 27806815 ref NP_776376.1 	plasminogen [Bos taurus] >gi 1...	174	1e-41	
gi 34878557 ref XP_224872.2 	similar to coagulation factor ...	174	1e-41	
gi 54636853 qb EAL26256.1 	GA15058-PA [Drosophila pseudoobs...	174	1e-41	

gi 41055921 ref NP_956439.1 	similar to adrenal secretory s...	174	1e-41	G
gi 47227752 emb CAG08915.1 	unnamed protein product [Tetrao...	174	1e-41	
gi 6435717 pdb 1QRZ D	Chain D, Catalytic Domain Of Plasmino...	174	1e-41	S
gi 57088539 ref XP_547173.1 	PREDICTED: similar to EOS prot...	173	2e-41	
gi 55732953 emb CAH93164.1 	hypothetical protein [Pongo pyg...	173	2e-41	
gi 27573762 pdb 1L4Z A	Chain A, X-Ray Crystal Structure Of ...	173	2e-41	S
gi 27573760 pdb 1L4D A	Chain A, Crystal Structure Of Microp...	173	2e-41	S
gi 7245727 pdb 1DDJ D	Chain D, Crystal Structure Of Human P...	173	2e-41	S
gi 5821851 pdb 1BML B	Chain B, Complex Of The Catalytic Dom...	173	2e-41	S
gi 130314 sp P80009 PLMN CANFA	Plasminogen	173	2e-41	
gi 57031802 ref XP_533468.1 	PREDICTED: hypothetical protei...	173	2e-41	
gi 31242535 ref XP_321698.1 	ENSANGP00000015747 [Anopheles ...	173	2e-41	G
gi 47523468 ref NP_999356.1 	tryptase [Sus scrofa] >gi 1820...	173	2e-41	G
gi 56967288 pdb 1XX9 B	Chain B, Crystal Structure Of The Fx...	173	2e-41	S
gi 10441463 gb AAG17054.1 	channel activating protease 1 [M...	173	2e-41	G
gi 1698668 gb AAB37261.1 	late trypsin precursor [Culex pip...	173	2e-41	
gi 13633203 sp Q9ESD1 PSS8 MOUSE	Prostasin precursor (Chann...	173	2e-41	
gi 130315 sp P80010 PLMN HORSE	Plasminogen	172	3e-41	
gi 52219018 ref NP_001004582.1 	zgc:92292 [Danio rerio] >gi...	172	3e-41	G
gi 13898841 gb AAK48894.1 	CUB-serine protease [Panulirus a...	172	3e-41	
gi 5564 emb CAA45715.1 	put. trypsin [Aedes aegypti] >gi 67...	172	3e-41	
gi 3006086 emb CAA75311.1 	trypsin [Litopenaeus vannamei]	172	3e-41	
gi 2118100 pir A61545	plasmin (EC 3.4.21.7) precursor - ho...	172	3e-41	
gi 15042732 gb AAK82432.1 	factor XI [Oryctolagus cuniculus]	172	3e-41	
gi 5295890 emb CAB46014.1 	plasminogen protein [Rattus norv...	172	4e-41	G
gi 57086269 ref XP_546520.1 	PREDICTED: similar to transmem...	172	4e-41	
gi 32402373 gb AAP81159.1 	trypsinogen [Pangasius hypophtha...	172	4e-41	
gi 55240943 gb EAA09162.2 	ENSANGP00000011601 [Anopheles ga...	172	4e-41	
gi 48098822 ref XP_394832.1 	similar to ENSANGP00000012201 ...	172	4e-41	G
gi 47222714 emb CAG00148.1 	unnamed protein product [Tetrao...	172	4e-41	
gi 2815616 gb AAB97886.1 	apolipoprotein a [Papio hamadryas]	172	4e-41	
gi 56967297 pdb 1XXF B	Chain B, Crystal Structure Of The Fx...	172	5e-41	S
gi 19922714 ref NP_611611.1 	CG4386-PA [Drosophila melanoga...	171	7e-41	G
gi 52139088 gb AAH82670.1 	Xesp-1 protein [Xenopus laevis]	171	7e-41	G
gi 1272431 gb AAA97479.1 	Astrypl	171	7e-41	
gi 39654880 pdb 1RJX B	Chain B, Human Plasminogen Catalytic...	171	7e-41	S
gi 67597 pir KFBO	coagulation factor IXa (EC 3.4.21.22) pr...	171	9e-41	
gi 38372173 sp Q95ND7 FA9 PANTR	Coagulation factor IX precu...	171	9e-41	
gi 2134456 pir I46260	plasmin (EC 3.4.21.7) precursor - we...	171	9e-41	
gi 86639 pir B30848	plasmin (EC 3.4.21.7) precursor - rhes...	171	1e-40	
gi 57097943 ref XP_532836.1 	PREDICTED: similar to Coagulat...	171	1e-40	
gi 56270387 gb AAH87611.1 	Unknown (protein for MGC:97869) ...	171	1e-40	
gi 67596 pir KFHU	coagulation factor IXa (EC 3.4.21.22) pr...	170	1e-40	G
gi 47216479 emb CAG02130.1 	unnamed protein product [Tetrao...	170	1e-40	
gi 6650672 gb AAF21966.1 	heart specific serine proteinase ...	170	1e-40	G
gi 4503649 ref NP_000124.1 	coagulation factor IX [Homo sap...	169	2e-40	G
gi 9757698 dbj BAB08216.1 	embryonic serine protease-1 [Xen...	169	2e-40	G
gi 57087141 ref XP_536782.1 	PREDICTED: similar to chymotry...	169	3e-40	
gi 38512040 gb AAH61083.1 	Chymotrypsinogen B1 [Mus musculu...	169	3e-40	G
gi 50806652 ref XP_424472.1 	PREDICTED: similar to proacros...	169	3e-40	G
gi 4210804 emb CAA76929.1 	trypsin [Phaedon cochleariae]	169	3e-40	
gi 21703806 ref NP_663378.1 	transmembrane protease, serine...	169	4e-40	G

gi 45758733 gb AAS76646.1 	blood coagulation factor IX [Bos...	169	4e-40	G
gi 56710319 ref NP_001008665.1 	blood coagulation factor IX...	169	4e-40	
gi 50746887 ref XP_426329.1 	PREDICTED: similar to Compleme...	169	4e-40	G
gi 48140173 ref XP_397087.1 	similar to Astrypl [Apis melli...	169	4e-40	G
gi 5441859 dbj BAA82365.1 	chymotrypsinogen 1 [Paralichthys...	169	4e-40	
gi 34870498 ref XP_220222.2 	similar to serine protease [Ra...	168	6e-40	G
gi 54636854 gb EAL26257.1 	GA18150-PA [Drosophila pseudoobs...	168	6e-40	
gi 13385032 ref NP_079859.1 	chymotrypsinogen B1 [Mus muscu...	168	6e-40	G
gi 3559980 emb CAA06644.1 	serine protease [Rattus rattus]	168	6e-40	
gi 6572446 emb CAB63112.1 	serine protease [Pacifastacus le...	168	6e-40	
gi 182609 gb AAA98726.1 	factor IX	168	6e-40	G
gi 57088545 ref XP_547176.1 	PREDICTED: similar to protease...	168	7e-40	
gi 5525101 dbj BAA82522.1 	tunicate retinoic acid-inducible...	168	7e-40	
gi 56611133 gb AAH87787.1 	Unknown (protein for MGC:108057)...	167	9e-40	
gi 55637037 ref XP_508786.1 	PREDICTED: similar to Transmem...	167	9e-40	
gi 19698564 gb AAL93209.1 	early trypsin-like protein precu...	167	9e-40	
gi 6911219 gb AAF31436.1 	type II membrane serine protease ...	167	1e-39	G
gi 37182183 gb AAQ88894.1 	TMPS3 [Homo sapiens]	167	1e-39	G
gi 15451940 ref NP_063947.1 	transmembrane protease, serine...	167	1e-39	G
gi 5562 emb CAA45714.1 	put. trypsin [Aedes aegypti] >gi 67...	167	1e-39	
gi 26347427 dbj BAC37362.1 	unnamed protein product [Mus mu...	167	1e-39	G
gi 108088 pir A21195	chymotrypsin (EC 3.4.21.1) 2 precurs...	167	2e-39	
gi 105012 pir A32869	apolipoprotein(a) (EC 3.4.21.-) - rhe...	167	2e-39	
gi 12841192 dbj BAB25112.1 	unnamed protein product [Mus mu...	167	2e-39	G
gi 11545839 ref NP_071402.1 	protease, serine, 22 [Homo sap...	166	2e-39	G
gi 37181917 gb AAQ88762.1 	PRSS22 [Homo sapiens]	166	2e-39	G
gi 21070351 gb AAM34268.1 	early trypsin [Aedes aegypti]	166	2e-39	
gi 47212882 emb CAF90331.1 	unnamed protein product [Tetrao...	166	2e-39	
gi 2734092 gb AAB93671.1 	SP001LA [Homo sapiens]	166	2e-39	G
gi 30230633 gb AAP20885.1 	tryptase-6 [Mus musculus]	166	3e-39	G
gi 57164273 ref NP_001009412.1 	tryptase [Ovis aries] >gi 4...	166	3e-39	G
gi 31324554 ref NP_852142.1 	protease, serine, 21 [Rattus n...	166	3e-39	G
gi 55240925 gb EAA09284.2 	ENSANGP00000012216 [Anopheles ga...	166	3e-39	
gi 50979168 ref NP_001003323.1 	coagulation factor IX [Cani...	166	4e-39	G
gi 57105368 ref XP_543288.1 	PREDICTED: similar to nicotini...	166	4e-39	
gi 24581459 ref NP_722915.1 	CG31954-PA [Drosophila melanog...	166	4e-39	G
gi 41054047 ref NP_956180.1 	chymotrypsin C (caldecrin) [Da...	166	4e-39	G
gi 32698940 ref NP_872365.1 	hypothetical protein MGC57341 ...	166	4e-39	G
gi 49119431 gb AAH73506.1 	MGC82715 protein [Xenopus laevis]	166	4e-39	G
gi 56208061 emb CAI21060.1 	novel elastase protein (zgc:637...	166	4e-39	
gi 14009271 gb AAK50138.1 	early trypsin [Culex pipiens qui...	166	4e-39	
gi 67552 pir TRDG	trypsin (EC 3.4.21.4) precursor, anionic...	165	5e-39	
gi 5031885 ref NP_005568.1 	lipoprotein, Lp(a) [Homo sapien...	165	5e-39	G
gi 24648245 ref NP_650825.1 	CG7432-PA [Drosophila melanoga...	165	5e-39	G
gi 55237399 gb EAL39600.1 	ENSANGP00000026990 [Anopheles ga...	165	5e-39	
gi 56203915 emb CAI22905.1 	LPA [Homo sapiens] >gi 55665907...	165	5e-39	
gi 559508 emb CAA57701.1 	trypsin [Paranotothenia magellani...	165	5e-39	
gi 48098409 ref XP_394066.1 	similar to CG9372-PA [Apis mel...	165	5e-39	G
gi 225794 prf 1313352A	apolipoprotein a	165	5e-39	
gi 6978717 ref NP_036668.1 	Chymotrypsinogen B [Rattus norv...	165	6e-39	G
gi 410329 emb CAA80518.1 	trypsin [Anopheles gambiae] >gi 3...	165	6e-39	

gi 11527822 gb AAG37012.1 	serine protease TADG12 [Homo sap...	165	6e-39	
gi 20142081 dbj BAB88920.1 	complement control protein fact...	165	6e-39	
gi 56681219 gb AAW21246.1 	digestive serine protease II [Ma...	164	8e-39	
gi 4098568 gb AAD00320.1 	plasminogen activator SPA [Scolop...	164	8e-39	
gi 5441853 dbj BAA82362.1 	trypsinogen 1 [Paralichthys oliv...	164	8e-39	
gi 21614531 ref NP_659205.1 	testisin isoform 2 [Homo sapie...	164	1e-38	
gi 54639795 gb EAL29197.1 	GA20347-PA [Drosophila pseudoobs...	164	1e-38	
gi 48130450 ref XP_393316.1 	similar to CG8213-PA [Apis mel...	164	1e-38	
gi 47220856 emb CAG00063.1 	unnamed protein product [Tetrao...	164	1e-38	
gi 47214192 emb CAG00820.1 	unnamed protein product [Tetrao...	164	1e-38	
gi 4753837 emb CAB41989.1 	tryptase [Ovis aries] >gi 182036...	164	1e-38	
gi 67550 pir TRPGTR	trypsin (EC 3.4.21.4) precursor - pig ...	164	1e-38	
gi 13516893 dbj BAB40330.1 	trypsinogen II [Engraulis japon...	164	1e-38	
gi 5822391 pdb 1RFN A	Chain A, Human Coagulation Factor Ixa...	164	1e-38	
gi 11055972 ref NP_065233.2 	tryptase 4 [Mus musculus] >gi ...	163	2e-38	
gi 17538534 ref NP_501379.1 	serine protease 22D (4I977) [C...	163	2e-38	
gi 29612490 gb AAH49588.1 	Prss21 protein [Mus musculus]	163	2e-38	
gi 5441855 dbj BAA82363.1 	trypsinogen 2 [Paralichthys oliv...	163	2e-38	
gi 1363091 pir S56160	mast cell tryptase precursor - Mongo...	163	2e-38	
gi 54645028 gb EAL33768.1 	GA16585-PA [Drosophila pseudoobs...	163	2e-38	
gi 51247093 pdb 1H9I E	Chain E, Complex Of Eeti-Ii Mutant W...	163	2e-38	
gi 47214193 emb CAG00821.1 	unnamed protein product [Tetrao...	163	2e-38	
gi 10835849 pdb 1FNI A	Chain A, Crystal Structure Of Porcin...	163	2e-38	
gi 4506147 ref NP_002761.1 	protease, serine, 2 preproprote...	162	3e-38	
gi 33126583 gb AAL14244.1 	protease serine 2 isoform B [Hom...	162	3e-38	
gi 16758930 ref NP_446461.1 	chymotrypsin-like [Rattus norv...	162	3e-38	
gi 47086795 ref NP_997783.1 	chymotrypsinogen B1 [Danio rer...	162	3e-38	
gi 50604052 gb AAH78367.1 	Unknown (protein for IMAGE:70385...	162	3e-38	
gi 3318722 pdb 1AN1 E	Chain E, Leech-Derived Tryptase Inhib...	162	3e-38	
gi 64386 emb CAA49678.1 	trypsin II [Salmo salar] >gi 42258...	162	4e-38	
gi 27465583 ref NP_775150.1 	cationic trypsinogen [Rattus n...	162	4e-38	
gi 31238307 ref XP_319744.1 	ENSANGP00000017160 [Anopheles ...	162	4e-38	
gi 45550384 ref NP_610435.3 	CG8213-PA [Drosophila melanoga...	162	4e-38	
gi 55235308 gb EAA14903.2 	ENSANGP00000017160 [Anopheles ga...	162	4e-38	
gi 18447345 gb AAL68238.1 	LD43328p [Drosophila melanogaster]	162	4e-38	
gi 13094662 gb AAK11956.1 	neonatal thrombolytic agent alph...	162	4e-38	
gi 19354409 gb AAH24374.1 	Mcpt6 protein [Mus musculus] >gi...	162	5e-38	
gi 37183186 gb AAQ89393.1 	PRSS21 [Homo sapiens] >gi 580319...	162	5e-38	
gi 30583551 gb AAP36020.1 	chymotrypsinogen B1 [Homo sapien...	162	5e-38	
gi 56972040 gb AAH87918.1 	Chymotrypsin-like [Mus musculus]...	162	5e-38	
gi 30584037 gb AAP36267.1 	Homo sapiens chymotrypsinogen B1...	162	5e-38	
gi 54641961 gb EAL30710.1 	GA18522-PA [Drosophila pseudoobs...	162	5e-38	
gi 23593662 ref XP_128541.2 	RIKEN cDNA 4931440B09 [Mus mus...	162	5e-38	
gi 47220857 emb CAG00064.1 	unnamed protein product [Tetrao...	162	5e-38	
gi 2443296 dbj BAA22400.1 	26kDa protease [Sarcophaga pereg...	162	5e-38	
gi 12843559 dbj BAB26029.1 	unnamed protein product [Mus mu...	162	5e-38	
gi 32394742 gb AAM96942.1 	trypsin 3 [Phlebotomus papatasi]	161	7e-38	
gi 28274638 gb AAO34406.1 	tissue plasminogen activator; TP...	161	7e-38	
gi 42543835 pdb 1UTM A	Chain A, Trypsin Specificity As Eluc...	161	7e-38	
gi 13183620 gb AAK15274.1 	sea star regeneration-associated...	161	7e-38	
gi 971196 gb AAA75001.1 	trypsinogen	161	7e-38	

gi 34784896 qb AAH56849.1 	MGC64417 protein [Xenopus laevis]	161	9e-38	G
gi 34866384 ref XP_217270.2 	similar to testis serine prote...	161	9e-38	G
gi 57097397 ref XP_532744.1 	PREDICTED: similar to trypsin ...	161	9e-38	
gi 56681217 qb AAW21245.1 	digestive serine protease I [May...	160	1e-37	
gi 14702169 ref NP_127509.1 	plasminogen activator, tissue ...	160	1e-37	G
gi 423498 pir A47246	tryptase (EC 3.4.21.59) 2 - mouse >gi...	160	1e-37	G
gi 441174 dbj BAA00881.1 	tissue plasminogen activator [Hom...	160	1e-37	G
gi 4505861 ref NP_000921.1 	plasminogen activator, tissue t...	160	1e-37	G
gi 33877196 qb AAH02795.2 	PLAT protein [Homo sapiens]	160	1e-37	G
gi 33872180 qb AAH18636.2 	PLAT protein [Homo sapiens] >gi ...	160	1e-37	G
gi 21357887 ref NP_648711.1 	CG4914-PA [Drosophila melanoga...	160	1e-37	G
gi 30583865 qb AAP36181.1 	Homo sapiens plasminogen activat...	160	1e-37	
gi 55630632 ref XP_528120.1 	PREDICTED: similar to PLAT pro...	160	1e-37	
gi 31981624 ref NP_112464.2 	mast cell protease 7 [Mus musc...	160	1e-37	G
gi 52551331 qb AAU84664.1 	trypsin [Oreochromis niloticus]	160	1e-37	
gi 339834 qb AAB59510.1 	plasminogen activator [Homo sapiens]	160	1e-37	G
gi 67572 pir KYBOB	chymotrypsin (EC 3.4.21.1) B precursor ...	160	1e-37	G
gi 785035 emb CAA60129.1 	trypsin [Litopenaeus vannamei] >g...	160	1e-37	
gi 3006082 emb CAA75309.1 	trypsin [Litopenaeus vannamei]	160	1e-37	
gi 57415 emb CAA41752.1 	trypsin V b-form [Rattus rattus] >...	160	2e-37	
gi 55631590 ref XP_528278.1 	PREDICTED: similar to tryptoph...	160	2e-37	
gi 54641711 qb EAL30461.1 	GA21737-PA [Drosophila pseudoobs...	160	2e-37	
gi 49115873 qb AAH73613.1 	MGC82927 protein [Xenopus laevis]	160	2e-37	G
gi 50753637 ref XP_425105.1 	PREDICTED: similar to chymotry...	160	2e-37	G
gi 5921501 emb CAB56465.1 	distal intestinal serine proteas...	160	2e-37	G
gi 38383098 qb AAH62334.1 	Unknown (protein for MGC:71136) ...	160	2e-37	G
gi 34868742 ref XP_220209.2 	similar to tryptase 5 [Rattus ...	160	2e-37	G
gi 56971185 qb AAH88769.1 	Unknown (protein for MGC:108128)...	160	2e-37	
gi 20988034 qb AAH30260.1 	PRSS2 protein [Homo sapiens]	160	2e-37	G
gi 54645404 qb EAL34144.1 	GA17401-PA [Drosophila pseudoobs...	160	2e-37	
gi 47132444 qb AAT11803.1 	pancreatic trypsinogen [Struthio...	160	2e-37	
gi 26006097 dbj BAC41392.1 	anionic trypsin [Oncorhynchus k...	160	2e-37	
gi 39587498 emb CAE58436.1 	Hypothetical protein CBG01571 [...	160	2e-37	
gi 27710074 ref XP_231718.1 	similar to Trypsin V-A precurs...	159	3e-37	G
gi 31207113 ref XP_312523.1 	ENSANGP00000014938 [Anopheles ...	159	3e-37	G
gi 23097244 ref NP_690851.1 	protease, serine, 33 [Homo sap...	159	3e-37	G
gi 24581698 ref NP_608848.1 	CG3355-PA [Drosophila melanoga...	159	3e-37	G
gi 33126535 qb AAL14243.1 	protease serine 4 isoform B [Hom...	159	3e-37	
gi 21536452 ref NP_002762.2 	mesotrypsin preproprotein [Hom...	159	3e-37	G
gi 55242354 qb EAA07518.2 	ENSANGP00000014938 [Anopheles ga...	159	3e-37	
gi 52551333 qb AAU84665.1 	trypsin [Oreochromis aureus]	159	3e-37	
gi 20988417 qb AAH30238.1 	Unknown (protein for IMAGE:45379...	159	3e-37	G
gi 33416522 qb AAH55854.1 	Protease, serine, 22 [Mus musculus]	159	3e-37	G
gi 13516891 dbj BAB40329.1 	trypsinogen [Engraulis japonicus]	159	3e-37	
gi 4868339 qb AAD31269.1 	trypsinogen RdoT3 precursor [Rhyz...	159	3e-37	
gi 6066378 emb CAB58178.1 	trypsinogen IV a-form [Homo sapi...	159	3e-37	G
gi 3452120 qb AAC32752.1 	trypsinogen 2 precursor [Pseudopl...	159	3e-37	
gi 7960528 emb CAB91840.1 	serine protease [Anopheles gambiae]	159	3e-37	
gi 423134 pir S33496	trypsin (EC 3.4.21.4) IV form a - hum...	159	3e-37	G
gi 6980535 pdb 2STB E	Chain E, Anionic Salmon Trypsin In Co...	159	3e-37	S
gi 57086241 ref XP_546505.1 	PREDICTED: similar to Transmem...	159	3e-37	

gi 47078378 gb AAT09850.1 	trypsin-like serine proteinase [...]	159	3e-37	
gi 2305256 gb AAB65760.1 	plasminogen [Macropus eugenii] >g...	159	3e-37	
gi 1827742 pdb 1PFX C	Chain C, Porcine Factor Ixa	159	3e-37	S
gi 55644525 ref XP_523475.1 	PREDICTED: similar to TPS1 pro...	159	4e-37	
gi 3006084 emb CAA75310.1 	trypsin [Litopenaeus vannamei]	159	4e-37	
gi 41350551 gb AAS00516.1 	trypsin [Oreochromis aureus]	159	4e-37	
gi 51473039 ref XP_496169.1 	PREDICTED: similar to Chymotry...	158	6e-37	G
gi 1552516 gb AAC80208.1 	trypsinogen C [Homo sapiens]	158	6e-37	
gi 64382 emb CAA49676.1 	trypsin IA [Salmo salar] >gi 42258...	158	6e-37	
gi 64380 emb CAA49680.1 	trypsin I [Salmo salar] >gi 422581...	158	6e-37	
gi 6981420 ref NP_036767.1 	pancreatic trypsin 1 [Rattus no...	158	6e-37	G
gi 19353198 gb AAH24903.1 	Prss32 protein [Mus musculus]	158	6e-37	G
gi 49256410 gb AAH73145.1 	CTRB1 protein [Homo sapiens]	158	6e-37	
gi 24496768 ref NP_038949.2 	transmembrane protease, serine...	158	6e-37	G
gi 30704873 gb AAH51852.1 	TPSAB1 protein [Homo sapiens]	158	6e-37	G
gi 20380845 gb AAH28059.1 	TPSAB1 protein [Homo sapiens] >g...	158	6e-37	G
gi 20899030 ref XP_128466.1 	tryptase 5 [Mus musculus]	158	6e-37	G
gi 51711962 ref XP_487918.1 	PREDICTED: similar to trypsino...	158	6e-37	G
gi 51010909 ref NP_001003405.1 	RIKEN cDNA 1810049H19 gene ...	158	6e-37	G
gi 468751 emb CAA55242.1 	chymotrypsin; prechymotrypsinogen...	158	6e-37	
gi 809221 pdb 1BIT 	The Crystal Structure Of Anionic Salmo...	158	6e-37	S
gi 47225581 emb CAG12064.1 	unnamed protein product [Tetrao...	158	6e-37	
gi 30421098 gb AAP23216.1 	tryptase 5 [Mus musculus]	158	6e-37	G
gi 18158713 pdb 1HJ8 A	Chain A, 1.00 Aa Trypsin From Atlant...	158	6e-37	S
gi 24582982 ref NP_523518.2 	CG9564-PA [Drosophila melanoga...	158	8e-37	G
gi 57162224 emb CAI39655.1 	OTTHUMP00000045395 [Homo sapien...	158	8e-37	
gi 38678694 gb AAR26346.1 	factor IX [Felis catus] >gi 5716...	158	8e-37	
gi 37182852 gb AAQ89226.1 	tryptophan/serine protease [Homo...	158	8e-37	G
gi 47086363 ref NP_998000.1 	elastase 2 like [Danio rerio] ...	158	8e-37	G
gi 45383277 ref NP_989773.1 	coagulation factor VII [Gallus...	158	8e-37	G
gi 48098818 ref XP_394830.1 	similar to CG4914-PA [Apis mel...	158	8e-37	G
gi 14270123 dbj BAB58886.1 	coagulation factor XI [Pan trog...	158	8e-37	
gi 20149993 pdb 1H4W A	Chain A, Structure Of Human Trypsin ...	158	8e-37	S
gi 12840814 dbj BAB24967.1 	unnamed protein product [Mus mu...	158	8e-37	G

Alignments

☐ >gi|11415040|ref|NP_068813.1| **G** matriptase [Homo sapiens]
[gi|20988875|gb|AAH30532.1|](#) **G** Matriptase [Homo sapiens]
[gi|6647302|gb|AAD42765.2|](#) **G** matriptase [Homo sapiens]
[gi|6002714|gb|AAF00109.1|](#) **G** membrane-type serine protease 1 [Homo sapiens]
[gi|13124575|sp|Q9Y5Y6|ST14](#) **G** HUMAN **G** Suppressor of tumorigenicity 14 (Matriptase) (M
protease 1) (MT-SP1) (Prostamin) (Serine protease
TADG-15) (Tumor associated differentially-expressed
gene-15 protein)
Length = 855

Score = 1698 bits (4397), Expect = 0.0
Identities = 805/855 (94%), Positives = 805/855 (94%)

Query: 1 MGSDRARXXXXXXXXXXXXXXXXXNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWXXXXX 60
MGSDRAR YNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRW
Sbjct: 1 MGSDRARKGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAA 60

Query: 61 XXXXXXXXXXXXXXXXXXXXWHLQYRDVRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKV 120
WHLQYRDVRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKV
Sbjct: 61 VLIGLLLVLGIGFLVWHLQYRDVRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKV 120

Query: 121 KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXX 180
KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHL
Sbjct: 121 KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEERVVM 180

Query: 181 LPPRARS LKS FVVT SVVAFPTDSKT VQRTQDN SCS FGLHARGVELMRFTTPGFPDSPYPA 240
LPPRARS LKS FVVT SVVAFPTDSKT VQRTQDN SCS FGLHARGVELMRFTTPGFPDSPYPA
Sbjct: 181 LPPRARS LKS FVVT SVVAFPTDSKT VQRTQDN SCS FGLHARGVELMRFTTPGFPDSPYPA 240

Query: 241 HARCQWALRGDADSVLSLTFRSFDLASCDERGS DLVTYNTLS PME PHALVQLCGTYPPS 300
HARCQWALRGDADSVLSLTFRSFDLASCDERGS DLVTYNTLS PME PHALVQLCGTYPPS
Sbjct: 241 HARCQWALRGDADSVLSLTFRSFDLASCDERGS DLVTYNTLS PME PHALVQLCGTYPPS 300

Query: 301 YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN SPYYPGHY 360
YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN SPYYPGHY
Sbjct: 301 YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN SPYYPGHY 360

Query: 361 PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTC PKDYVE INGEKYCGERSQFVVT 420
PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTC PKDYVE INGEKYCGERSQFVVT
Sbjct: 361 PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTC PKDYVE INGEKYCGERSQFVVT 420

Query: 421 NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFT CRTGRCIRKELRCDGWADCTDH 480
NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFT CRTGRCIRKELRCDGWADCTDH
Sbjct: 421 NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFT CRTGRCIRKELRCDGWADCTDH 480

Query: 481 SDELNCSCDAGHQFTCKNKFCPLFWVCD SVNDCG DNSDEQGCSCPAQTFRCSNGKCLSK 540
SDELNCSCDAGHQFTCKNKFCPLFWVCD SVNDCG DNSDEQGCSCPAQTFRCSNGKCLSK
Sbjct: 481 SDELNCSCDAGHQFTCKNKFCPLFWVCD SVNDCG DNSDEQGCSCPAQTFRCSNGKCLSK 540

Query: 541 SQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCS DG SDEK 600
SQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCS DG SDEK
Sbjct: 541 SQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCS DG SDEK 600

Query: 601 DCDCGLRSFTRQARVVG GTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID 660
DCDCGLRSFTRQARVVG GTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID
Sbjct: 601 DCDCGLRSFTRQARVVG GTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID 660

Query: 661 DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP 720
DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
Sbjct: 661 DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP 720

Query: 721 AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTT CENLL 780
AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTT CENLL
Sbjct: 721 AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTT CENLL 780

Query: 781 PQQITPRMMCVGFLSGGVDSCQGD SGGPLSSVEADGRIFQAGV VSWG DGCAQRNKPGVYT 840
PQQITPRMMCVGFLSGGVDSCQGD SGGPLSSVEADGRIFQAGV VSWG DGCAQRNKPGVYT
Sbjct: 781 PQQITPRMMCVGFLSGGVDSCQGD SGGPLSSVEADGRIFQAGV VSWG DGCAQRNKPGVYT 840

Query: 841 RLPLFRDWIKENTGV 855

RLPLFRDWIKENTGV
Sbjct: 841 RLPLFRDWIKENTGV 855

☐ >gi|12249015|dbj|BAB20376.1| ☒ prostamin [Homo sapiens]
Length = 855

Score = 1696 bits (4393), Expect = 0.0
Identities = 804/855 (94%), Positives = 804/855 (94%)

```
Query: 1  MGSDRARXXXXXXXXXXXXXXXXXNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWXXXXX 60
          MGSDRAR                      YNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRW
Sbjct: 1  MGSDRARKGGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVVLAA 60

Query: 61  XXXXXXXXXXXXXXXXXXXXWHLQYRDVRVQKVFNQGYMRITNENFVDAYENSNSTEFVSLASKV 120
          WHLQYRDVRVQKVFNQGYMRITNENFVDAYENSNSTEFVSLASKV
Sbjct: 61  VLIGLLLVLGIGFLVWHLQYRDVRVQKVFNQGYMRITNENFVDAYENSNSTEFVSLASKV 120

Query: 121  KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYWSEFSIPQHLXXXXXXXXXXXXXXXXXXXXX 180
          KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYWSEFSIPQHL
Sbjct: 121  KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYWSEFSIPQHLVEEAERVMAEERVVM 180

Query: 181  LPPRARSLSKSFVVTSVVAFPTDSKTVQRTQDNCSFGLHARGVELMRFTTPGFPDSPYPA 240
          LPPRARSLSKSFVVTSVVAFPTDSKTVQRTQDNCSFGLHARGVELMRFTTPGFPDSPYPA
Sbjct: 181  LPPRARSLSKSFVVTSVVAFPTDSKTVQRTQDNCSFGLHARGVELMRFTTPGFPDSPYPA 240

Query: 241  HARCQWALRGDADSVLSLTFRSFDLASCDEGSDLVTVYNTLSPMEPHALVQLCGTYPPS 300
          HARCQWALRGDADSVLSLTFRSFDLASCDEGSDLVTVYNTLSPMEPHALVQLCGTYPPS
Sbjct: 241  HARCQWALRGDADSVLSLTFRSFDLASCDEGSDLVTVYNTLSPMEPHALVQLCGTYPPS 300

Query: 301  YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY 360
          YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
Sbjct: 301  YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY 360

Query: 361  PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTS 420
          PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTS
Sbjct: 361  PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTS 420

Query: 421  NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH 480
          NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH
Sbjct: 421  NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH 480

Query: 481  SDELNCSCDAGHQFTCKNKFKCKPLFWVCDNVDCGDNDSDEQGCSCPAQTFRCSNGKCLSK 540
          SDELNCSCDAGHQFTCKNKFKCKPLFWVCDNVDCGDNDSDEQGCSCPAQTFRCSNGKCLSK
Sbjct: 481  SDELNCSCDAGHQFTCKNKFKCKPLFWVCDNVDCGDNDSDEQGCSCPAQTFRCSNGKCLSK 540

Query: 541  SQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSGDSDEK 600
          SQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSGDSDEK
Sbjct: 541  SQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSGDSDEK 600

Query: 601  DCDCGLRSFTRQARVVGTDADGEWVWQVSLHALGQGHICGASLISPNWLVSAAHCYID 660
          DCDCGLRSFTRQARVVGTDADGEWVWQVSLHALGQGHICGASLISPNWLVSAAHCYID
Sbjct: 601  DCDCGLRSFTRQARVVGTDADGEWVWQVSLHALGQGHICGASLISPNWLVSAAHCYID 660

Query: 661  DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP 720
          DRGFRYSDPTQWT FLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
Sbjct: 661  DRGFRYSDPTQWTVFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP 720

Query: 721  AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTTCENLL 780
```

AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCE
 Sbjct: 721 AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCE 780

Query: 781 PQQITPRMCMVGFLSGGVDSQGDSSGGLSSVEADGRIFQAGVVS
 PQQITPRMCMVGFLSGGVDSQGDSSGGLSSVEADGRIFQAGVVS
 Sbjct: 781 PQQITPRMCMVGFLSGGVDSQGDSSGGLSSVEADGRIFQAGVVS 840

Query: 841 RLPLFRDWIKENTGV 855
 RLPLFRDWIKENTGV
 Sbjct: 841 RLPLFRDWIKENTGV 855

☐ >gi|10257390|gb|AAG15395.1| ☒ serine protease TADG15 [Homo sapiens]
 Length = 855

Score = 1696 bits (4391), Expect = 0.0
 Identities = 804/855 (94%), Positives = 804/855 (94%)

Query: 1 MGSDRARXXXXXXXXXXXXXXXXXNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWXXXXX 60
 MGSDRAR YNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRW
 Sbjct: 1 MGSDRARKGGGPKDFGAGLKYNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWVLA 60

Query: 61 XXXXXXXXXXXXXXXXXXXXWHLQYRDVRVQKVFNMGYMRITNENFVDAYENSNSTEFVSLASKV 120
 WHLQYRDVRVQKVFNMGYMRITNENFVDAYENSNSTEFVSLASKV
 Sbjct: 61 VLIGLLLVLGIGFLVWHLQYRDVRVQKVFNMGYMRITNENFVDAYENSNSTEFVSLASKV 120

Query: 121 KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXX 180
 KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHL
 Sbjct: 121 KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEERVVM 180

Query: 181 LPPRARSLSKFVVTSVVAFPTDSKTQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA 240
 LPPRARSLSKFVVTSVVAFPTDSKTQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA
 Sbjct: 181 LPPRARSLSKFVVTSVVAFPTDSKTQRTQDNSCSFGLHARGVELMRFTTPGFPDSPYPA 240

Query: 241 HARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTYNTLSPMEPHALVQLCGTYPSP 300
 HARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTYNTLSPMEPHALVQLCGTYPSP
 Sbjct: 241 HARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTYNTLSPMEPHALVQLCGTYPSP 300

Query: 301 YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY 360
 YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY
 Sbjct: 301 YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHY 360

Query: 361 PPNIDCTWNIEVPNNQHVKVRFFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVT 420
 PPNIDCTWNIEVPNNQHVKVRFFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVT
 Sbjct: 361 PPNIDCTWNIEVPNNQHVKVSFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVT 420

Query: 421 NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH 480
 NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH
 Sbjct: 421 NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH 480

Query: 481 SDELNCSDAGHQFTCKNKFKCKPLFWVCDSVNDCGDNSEQGCSCPAQTFRCNSNGKCLSK 540
 SDELNCSDAGHQFTCKNKFKCKPLFWVCDSVNDCGDNSEQGCSCPAQTFRCNSNGKCLSK
 Sbjct: 481 SDELNCSDAGHQFTCKNKFKCKPLFWVCDSVNDCGDNSEQGCSCPAQTFRCNSNGKCLSK 540

Query: 541 SQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK 600
 SQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK
 Sbjct: 541 SQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK 600

Query: 601 DCDCLRSFTRQARVVGTDAGEGEWPQVSLHALGQGHICGASLISPNWLVSAAHCYID 660

DCDCGLRSFTRQARVVGTTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID
 Sbjct: 601 DCDCGLRSFTRQARVVGTTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYID 660

Query: 661 DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP 720
 DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP
 Sbjct: 661 DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP 720

Query: 721 AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTENLL 780
 AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTENLL
 Sbjct: 721 AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTENLL 780

Query: 781 PQQITPRMCMVGFLSGGVDSCQGDSSGGLSSVEADGRIFQAGVSWGDGCAQRNKPVGVT 840
 PQQITPRMCMVGFLSGGVDSCQGDSSGGLSSVEADGRIFQAGVSWGDGCAQRNKPVGVT
 Sbjct: 781 PQQITPRMCMVGFLSGGVDSCQGDSSGGLSSVEADGRIFQAGVSWGDGCAQRNKPVGVT 840

Query: 841 RLPLFRDWIKENTGV 855
 RLPLFRDWIKENTGV
 Sbjct: 841 RLPLFRDWIKENTGV 855

☐ >gi|55637345|ref|XP_508863.1| PREDICTED: similar to matriptase; suppression of t
 (colon carcinoma); membrane-type serine protease; serine
 protease TADG-15; tumor associated differentially
 expressed gene 15 protein [Pan troglodytes]
 Length = 1153

Score = 1444 bits (3739), Expect = 0.0
 Identities = 693/809 (85%), Positives = 705/809 (87%), Gaps = 29/809 (3%)

Query: 24 SRHEKVNGLLEEGVEFLPVNNVKKVEKHGPGRWXXXXXXXXXXXXXXXXXXXXXWHLQYRD 83
 S+ +KVNGLLEEGVEFLPVNNVKKVEKHGPGRW WHLQYRD
 Sbjct: 201 SKGKKVNGLLEEGVEFLPVNNVKKVEKHGPGRWVLA AVLIGLLLVLLGIGFLVWHLQYRD 260

Query: 84 VRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKESAV 143
 VRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKESAV
 Sbjct: 261 VRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKESAV 320

Query: 144 TAFSEGSVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXXXXXLPPRARSLSFVVTSVVAF---- 199
 TAFSEGSVIAYYWSEFSIPQHL LPPRARSLSFVVTSVVAF
 Sbjct: 321 TAFSEGSVIAYYWSEFSIPQHLVEEAERVMAEERVVMLPPRARSLSFVVTSVVAFRESE 380

Query: 200 -----PTDSKTQVQRTQDNSCSFGLHARGVELMRFTTPGFPDS 236
 TDSKTQVQRTQDNSCSFGLHARGVELMRFTTPGFPDS
 Sbjct: 381 GQGWAWDWPAPFHGEMLYSPSYSSATDSKTQVQRTQDNSCSFGLHARGVELMRFTTPGFPDS 440

Query: 237 PYPAHARCQWALRGDADSVLSLTFRSFDLASC DERGSDLVTYNTLSPEPHALVQLCGT 296
 PYPAHARCQWALRGDADSVLSLTFRSFDLASC DERGSDLV VYNTLSPEPHALVQLCGT
 Sbjct: 441 PYPAHARCQWALRGDADSVLSLTFRSFDLASC DERGSDLVMVYNTLSPEPHALVQLCGT 500

Query: 297 YPPSYNLTFFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGRLRKAQGTFNSPYY 356
 YPPSYNLTFFHSSQNVLL+TLITNT RRHPGFEATFFQLPRM SCGRLRKAQGTFNSPYY
 Sbjct: 501 YPPSYNLTFFHSSQNVLLVTLITNTRRRHPGFEATFFQLPRMRSCGRLRKAQGTFNSPYY 560

Query: 357 PGHYPPNIDCTWNIEVPNNQHVVRKFFFYLLPGVPAGTCPKDYVEINGEKYCGERSQF 416
 PGHYPPNIDCTWNIEVPNNQHVVRKFFFYLLPGVPAGTCPKDYVEINGEKYCGERSQF
 Sbjct: 561 PGHYPPNIDCTWNIEVPNNQHVVRKFFFYLLPGVPAGTCPKDYVEINGEKYCGERSQF 620

Query: 417 VVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTCRCIRKELRCDGWAD 476
 VVTSNSNKITVRFHSDQSYTDTGFLAEY+SYDSSDPCPGQFTCRTCRCIRKELRCDGWAD

Sbjct: 621 VVTSNSNKITVRFHSDQSYTDTGFLAEYVSYDSSDPCPGQFTCRTGRCIRKELRCDGWAD 680

Query: 477 CTDHSDELNCSCDAGHQFTCKNKFKCKPLFWVCDVNDGDNDEQGCSCPAQTFRCNSNGK 536
CTDHSDELNCSCDA HQFTCKNKFKCKPLFWVCDVNDGDNDEQGCSCPAQTFRCNSNGK

Sbjct: 681 CTDHSDELNCSCDASHQFTCKNKFKCKPLFWVCDVNDGDNDEQGCSCPAQTFRCNSNGK 740

Query: 537 CLSKSQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDG 596
CLSKSQQCNGKDDCGDGSDEASCP VNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDG

Sbjct: 741 CLSKSQQCNGKDDCGDGSDEASCPVTNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDG 800

Query: 597 SDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAH 656
SDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAH

Sbjct: 801 SDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAH 860

Query: 657 CYIDDRGFRYS DPTQWTAFLGLHDQS QRSAPGVQERRLKRIISHPFFNDFTFDYDIALLE 716
CYIDDRGFRYS DPTQWTAFLGLHDQS QRSAPGVQERRLKRIISHPFFNDFTFDYDIALLE

Sbjct: 861 CYIDDRGFRYS DPTQWTAFLGLHDQS QRSAPGVQERRLKRIISHPFFNDFTFDYDIALLE 920

Query: 717 LEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALI--LQKGEIRVINQT 774
LEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYG + L++ E Q

Sbjct: 921 LEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGAYAEHLSSLERKENEQDLQL 980

Query: 775 TCENLLPQQITPRMCMVGFLSGGVDSCQG 803
C + P+ + + +C G

Sbjct: 981 QCPHRTPRFAAPSLRLSASRSLTPACHG 1009

Score = 208 bits (530), Expect = 5e-52
Identities = 99/99 (100%), Positives = 99/99 (100%)

Query: 757 GTGALILQKGEIRVINQTTTCENLLPQQITPRMCMVGFLSGGVDSCQGDSSGGPLSSVEADG 816
GTGALILQKGEIRVINQTTTCENLLPQQITPRMCMVGFLSGGVDSCQGDSSGGPLSSVEADG

Sbjct: 1055 GTGALILQKGEIRVINQTTTCENLLPQQITPRMCMVGFLSGGVDSCQGDSSGGPLSSVEADG 1114

Query: 817 RIFQAGVVS WGDGCAQRNKPGVYTRLPLFRDWIKENTGV 855
RIFQAGVVS WGDGCAQRNKPGVYTRLPLFRDWIKENTGV

Sbjct: 1115 RIFQAGVVS WGDGCAQRNKPGVYTRLPLFRDWIKENTGV 1153

☐ >gi|7363445|ref|NP_035306.2| ☒ G suppression of tumorigenicity 14 (colon carcinoma
gi|13529566|gb|AAH05496.1| ☒ G Suppression of tumorigenicity 14 (colon carcinoma) [M
gi|7330638|gb|AAD02230.3| ☒ G epithin [Mus musculus]
gi|13959712|sp|P56677|ST14 MOUSE ☒ G Suppressor of tumorigenicity 14 (Epithin)
gi|26342937|dbj|BAC35125.1| ☒ G unnamed protein product [Mus musculus]
Length = 855

Score = 1438 bits (3722), Expect = 0.0
Identities = 668/855 (78%), Positives = 738/855 (86%)

Query: 1 MGSDRARXXXXXXXXXXXXXXXXXNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPRWXXXXX 60
MGS+R R YNSR E +NG EEGVEFLP NN KKVEK GP RW

Sbjct: 1 MGSNRGRKAGGGSQDFGAGLKYNSRLENMNGFEEGVEFLPANNAKKVEKGRPRRWVVLVA 60

Query: 61 XXXXXXXXXXXXXXXXXXXXWHLQYRDVRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKV 120
WH YR+VRVQKVFNG++RITNE F+DAYENS STEF+SLAS+V

Sbjct: 61 VLFSFLLLSLMAGLLVWHFHYRNVRVQKVFNGHLRITNEIFLDAYENSTSTEFISLASQV 120

Query: 121 KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXX 180
K+ALKLLY+ VP LGPYHK+SAVTAFSEGSVIAYYWSEFSIP HL

Sbjct: 121 KEALKLLYNEVPVLGPYHKSAVTAFSEGSVIAYYWSEFSIPPHLAEVDRAMAVERVVT 180

Query: 181 LPPRARSLKSFVVTSVVAFPTDSKTQRTQDNCSFGLHARGVELMRFTTPGFPDSPYPA 240
LPPRAR+LKSFV+TSVVAFP D + +QRTQDNCSF LHA G + RFTTPGFP+SPYPA

Sbjct: 181 LPPRARALKSFVLTSVVAFPIDPRMLQRTQDNCSFALHAHGAAVTRFTTPGFPNSPYPA 240

Query: 241 HARCQWALRGDADSVLSLTFRSFDLASCDERGSDDLVTVYNTLSPMEPHALVQLCGTYPSPS 300
HARCQW LRGDADSVLSLTFRSFD+A CDE GSDLVTVY++LSPMEPHA+V+LCGT+ PS

Sbjct: 241 HARCQWVLRGDADSVLSLTFRSFDVAPCDEHGSDDLVTVYDSLSPMEPHAVVRLCGTFSPS 300

Query: 301 YNLTFHSSQNVLLITLITNTERRHPGFEATFFQLPRMSSCGRLRKAQGTFNSPYYPGHY 360
YNLTF SSQNV L+TLITNT+RRHPGFEATFFQLP+MSSCGG L QGT+SPYYPGHY

Sbjct: 301 YNLTFHSSQNVFLVTLITNTDRRHHPGFEATFFQLPKMSSCGFLSDTQGTFSPPYYPGHY 360

Query: 361 PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCKDYVEINGEKYCGERSQFVVTS 420
PPNI+CTWNI+VPNN++VKVRFK FYL++P VP G+C KDYVEINGEKYCGERSQFVV+S

Sbjct: 361 PPNINCTWNIKVPNNRNKVRFKLFYLVDPNVPVGSCTKDYVEINGEKYCGERSQFVVSS 420

Query: 421 NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTTCRTGRCIRKELRCDGWADCTDH 480
NS+KITV FHSD SYTDTGFLAEYLSYDS+DPCPG F C+TGRCIRKELRCDGWADC D+

Sbjct: 421 NSSKITVHFHSDHSYTDTGFLAEYLSYDSNDPCPGMFMCKTGRCIRKELRCDGWADCPDY 480

Query: 481 SDEINCSCDAGHQFTCKNKFKPLFWVCDVNDGDNDEQGCSCPAQTFRCNKGKCLSK 540
SDE C C+A HQFTCKN+FCKPLFWVCDVNDGCD SDE+GCSCPA +F+CSNGKCL +

Sbjct: 481 SDERYCRNATHQFTCKNQFCKPLFWVCDVNDGDSDEEGCSCPAGSFKCSNGKCLPQ 540

Query: 541 SQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK 600
SQ+CNGKD+CGDGSDEASC VNVV+CTK+TYRC NGLCLSKGNPECDGK DCSDGSDEK

Sbjct: 541 SQQCNGKDNCGDGSDEASCDVNVVSCCKYTYRCQNGCLCLSKGNPECDGKDCSDGSDEK 600

Query: 601 CDCGLRSFTRQARVVGGTDADEGEWPQVSLHALGQGHICGASLISPNWLVSAAHCYID 660
+CDCGLRSFT+QARVVGGT+ADEGEWPQVSLHALGQGH+CGASLISP+WLVSAAHC+ D

Sbjct: 601 NCDGLRSFTKQARVVGGTNADEGEWPQVSLHALGQGHLCGASLISPDWLVSAAHCFQD 660

Query: 661 DRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP 720
D+ F+YSD T WTAFLGL DQS+RSA GVQE +LKRII+HP FNDFTFDYDIALLELEK

Sbjct: 661 DKNFKYSYDTMWTAFLGLLDQSKRSASGVQELKLKRIITHPSFNDFTFDYDIALLELEKS 720

Query: 721 AEYSSMRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTTCENLL 780
EYS++VRPICLPDA+HVFPAGKAIWVTGWGHT+ GGTGALILQKGEIRVINQTTTCE+L+

Sbjct: 721 VEYSTVVRPICLPDATHVFPAGKAIWVTGWGHTKEGGTGALILQKGEIRVINQTTCEDLM 780

Query: 781 PQQITPRMMC VGFLSGVDSCQGDSSGGLSSVEADGRIFQAGVVS WGDCGAQRNKPGVYT 840
PQQITPRMMC VGFLSGVDSCQGDSSGGLSS E DGR+FQAGVVS WG+GCAQRNKPGVYT

Sbjct: 781 PQQITPRMMC VGFLSGVDSCQGDSSGGLSSAEKDGRMFQAGVVS WGECAQRNKPGVYT 840

Query: 841 RLPLFRDWIKENTGV 855
RLP+ RDWIKE+TGV

Sbjct: 841 RLPVVRDWIKEHTGV 855

☐ >gi|16758444|ref|NP_446087.1| ☒ suppression of tumorigenicity 14 [Rattus norvegicus]
gi|25527058|pir||JC7775 membrane type-serine protease 1 - rat
gi|25518264|pir||JC7731 membrane-bound arginine-specific serine proteinase precursor
gi|9650964|dbj|BAB03502.1| ☒ membrane bound serine protease [Rattus norvegicus]

gi|10336527|dbj|BAB13765.1| **G** membrane bound arginine specific serine protease [Ra
norvegicus]
Length = 855

Score = 1433 bits (3710), Expect = 0.0
Identities = 664/855 (77%), Positives = 738/855 (86%)

```
Query: 1  MGSDRARXXXXXXXXXXXXXXXXXNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWXXXXX 60
      MG++R R                      YNSR E +NG EEGVEFLPVNN K+VEK GP RW
Sbjct: 1  MGNNRGRKAGGGSQDFGAGLKYNSRLENMNGFEEGVEFLPVNNAKQVEKRGPRRWVMVA 60

Query: 61  XXXXXXXXXXXXXXXXXXXXWHLQYRDVRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKV 120
      WH YR+VR+QKVFNG++RITNENF+DAYENS STEF+SLAS+V
Sbjct: 61  VVFSLLLLSLMAGLLVWHFHYNVRIQKVFNGHLRITNENFLDAYENSTSTEFISLASQV 120

Query: 121  KDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXX 180
      K+ALKL+YS VP LGPYHK+S VTAFSEGSVIAYYWSEFSIP HL
Sbjct: 121  KEALKLMYSEVPVLGPYHKKSTVTAFSEGSVIAYYWSEFSIPPHLEEEVDRAVERVVT 180

Query: 181  LPPRARSLKSFVVTSVVAFPTDSKTVQRTQDNCSFGLHARGVELMRFTTPGFPDSPYPA 240
      LPPRAR+LKSFV+TSVVAFP D + +QRTQDNCSF LHARG + RFTTPGFP+SPYPA
Sbjct: 181  LPPRARALKSFVLTSVVAFPIDPRMLQRTQDNCSFALHARGRTVTRFTTPGFPNSPYPA 240

Query: 241  HARCQWALRGDADSVLSLTFRSFDLASCDERGSIDLVTYNTLSPEPHALVQLCGTYPPS 300
      HARCQW LRGDADSVLSLTFRSFD+A CD SDLVTYV++LSPMEPHA+V+LCGT+ PS
Sbjct: 241  HARCQWVLRGDADSVLSLTFRSFDVAPCDGHSDSLVTYVDSLSPMEPHAVVRLCGTFSPS 300

Query: 301  YNLTFHSSQNVLITLITNTERRHPGFEATFFQLPRMSSCGRLRKAQGTFNSPYYPGHY 360
      YNLTF SSQNV L+TLITNT+RRHPGFEATFFQLP+MSSCGG L +AQGTF+SPYYPGHY
Sbjct: 301  YNLTFLLSSQNVFLVTLITNTDRRHPGFEATFFQLPKMSSCGLLSEAQGTFFSPYYPGHY 360

Query: 361  PPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCKPDYVEINGEKYCGERSQFVVT 420
      PPNI+CTWNI+VPNN++VKVRFK FYL++P +P G+C KDYVEINGEK+CGERSQFVV+S
Sbjct: 361  PPNINCTWNIKVPNNRNVKVRFKLFYLVDPNI PVGSCTKDYVEINGEKFCGERSQFVVSS 420

Query: 421  NSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDH 480
      NS+KITV FHSD SYTDTGFLAEYLSYDS+DPCPG F C+TGRCIRK+LRCDGWADC D+
Sbjct: 421  NSSKITVHFHSDHSYTDTGFLAEYLSYDSNDPCPGMFMCKTGRCIRKDLRCDGWADCPDY 480

Query: 481  SDELNCSCDAGHQFTCKNKFCPLFWVCDSVNDCGDSDEQGCSCPAQTFRCNSNGKCLSK 540
      SDE +C C+A HQF CKN+FCKPLFWVCDSVNDCGD SDE+GCSCPA +F+CSNGKCL +
Sbjct: 481  SDERHCRCNATHQFMCKNQFCKPLFWVCDSVNDCGDSDEEGCSCPAGSFKCSNGKCLPQ 540

Query: 541  SQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSGDSDEK 600
      SQQCNGKDDCGDGSDEASC VN V+CTK+TYRC NGLCL+KGNPECDGK+DCSDGDSDEK
Sbjct: 541  SQQCNGKDDCGDGSDEASCDNVNAVSCTKYTYRCQNGLCNLKGNPECDGKKDCSDGDSDEK 600

Query: 601  CDCGLRSFTRQARVVGTTDADEGEWPWQVSLHALGQGHICGASLISPWLVSAAHCYID 660
      +CDCGLRSFT+QARVVGTT+ADEGEWPWQVSLHALGQGH+CGASLISP+WLVSAAHC+ D
Sbjct: 601  NCDGLRSFTKQARVVGTTNADEGEWPWQVSLHALGQGHLCGASLISPDLVLSAAHCFQD 660

Query: 661  DRGFRYSIPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKP 720
      + F+YS D T WTAFLGL DQS+RSA GVQE +LKRII+HP FNDFTFDYDIALLELEKP
Sbjct: 661  ETIFKYSIDHTMWTAFLGLLDQSKRSASGVQEHKLKRIITHPSFNDFTFDYDIALLELEKP 720

Query: 721  AEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCEPLL 780
      AEYS++VRPICLPD +HVFPAGKAIWVTGWGHT+ GGTGALILQKGEIRVINQTTCE LL
Sbjct: 721  AEYSTVVRPICLPDNTHVFPAGKAIWVTGWGHTKEGGTGALILQKGEIRVINQTTCEELL 780

Query: 781  PQQITPRMMCVGFLSGGVDSQGDSSGGLSSVEADGRIFQAGVVSWDGCAQRNKPQVYT 840
```

PQQITPRMCMVGFLSGGVDSCQGDSSGGPLSSVE DGRIFQAGVVSWSG+GCAQRNKPVGVT
 Sbjct: 781 PQQITPRMCMVGFLSGGVDSCQGDSSGGPLSSVEKDGRIFQAGVVSWSGEGCAQRNKPVGVT 840

Query: 841 RLPLFRDWIKENTGV 855
 R+P RDWIKE TGV
 Sbjct: 841 RIPEVRDWIKEQTGV 855

☐ >gi|34782939|gb|AAH05826.2| ☒ ST14 protein [Homo sapiens]
 Length = 526

Score = 1145 bits (2962), Expect = 0.0
 Identities = 526/526 (100%), Positives = 526/526 (100%)

Query: 330 TFFQLPRMSSCGGRLRKAQGTFTNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRKFFFYLL 389
 TFFQLPRMSSCGGRLRKAQGTFTNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRKFFFYLL
 Sbjct: 1 TFFQLPRMSSCGGRLRKAQGTFTNSPYYPGHYPPNIDCTWNIEVPNNQHVKVRKFFFYLL 60

Query: 390 PGVPAGTCPKDYVEINGEKYCGERSQFVVTSSNSNKITVRFHSDQSYTDTGFLAEYLSYDS 449
 PGVPAGTCPKDYVEINGEKYCGERSQFVVTSSNSNKITVRFHSDQSYTDTGFLAEYLSYDS
 Sbjct: 61 PGVPAGTCPKDYVEINGEKYCGERSQFVVTSSNSNKITVRFHSDQSYTDTGFLAEYLSYDS 120

Query: 450 SDPCPGQFTTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCCKPLFWVCD 509
 SDPCPGQFTTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCCKPLFWVCD
 Sbjct: 121 SDPCPGQFTTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCCKPLFWVCD 180

Query: 510 SVNDCGDNDSDEQGCSCPAQTFRCSSNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVTCTK 569
 SVNDCGDNDSDEQGCSCPAQTFRCSSNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVTCTK
 Sbjct: 181 SVNDCGDNDSDEQGCSCPAQTFRCSSNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVTCTK 240

Query: 570 HTYRCLNGLCLSKGNPECDGKEDCSGDSDEKDCDCGLRSFTRQARVVGGTDADEGEWFPWQ 629
 HTYRCLNGLCLSKGNPECDGKEDCSGDSDEKDCDCGLRSFTRQARVVGGTDADEGEWFPWQ
 Sbjct: 241 HTYRCLNGLCLSKGNPECDGKEDCSGDSDEKDCDCGLRSFTRQARVVGGTDADEGEWFPWQ 300

Query: 630 VSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGV 689
 VSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGV
 Sbjct: 301 VSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGV 360

Query: 690 QERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTG 749
 QERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTG
 Sbjct: 361 QERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTG 420

Query: 750 WGHTQYGGTGALILQKGEIRVINQTTNENLLPQQITPRMCMVGFLSGGVDSCQGDSSGGPL 809
 WGHTQYGGTGALILQKGEIRVINQTTNENLLPQQITPRMCMVGFLSGGVDSCQGDSSGGPL
 Sbjct: 421 WGHTQYGGTGALILQKGEIRVINQTTNENLLPQQITPRMCMVGFLSGGVDSCQGDSSGGPL 480

Query: 810 SSVEADGRIFQAGVVSWSGDGCAQRNKPVGVTTRLPLFRDWIKENTGV 855
 SSVEADGRIFQAGVVSWSGDGCAQRNKPVGVTTRLPLFRDWIKENTGV
 Sbjct: 481 SSVEADGRIFQAGVVSWSGDGCAQRNKPVGVTTRLPLFRDWIKENTGV 526

☐ >gi|50760033|ref|XP_417872.1| ☒ PREDICTED: similar to suppression of tumorigenic
 of tumorigenicity 14 (colon carcinoma, matriptase,
 epithin); suppression of tumorigenicity 14 (colon
 carcinoma); suppression of tumorigenicity 14 (colon
 carcinoma matriptase epithin); membran... [Gallus gallus]
 Length = 1325

Score = 1095 bits (2832), Expect = 0.0
Identities = 504/833 (60%), Positives = 623/833 (74%), Gaps = 7/833 (0%)

Query: 27 EKVNGLEEGVEFLPVNNVKKVEKHGPGRWXXXXXXXXXXXXXXXXXXXXXWHLQYRDVRV 86
+ +N LEEGVEFLP N KK+EK GP R WH +YR+ V
Sbjct: 496 QDMNNLEEGVEFLPAMNSKKMEKRGPKRRVVVAILIIAFLLLISLVTGLLVWHFKYRNAPV 555

Query: 87 QKVFNNGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKESAVTAF 146
QKVF G++R+ N F+DAYENS+S EF+ LA KVK ++ +Y P +GPYHKE+ +TAF
Sbjct: 556 QKVFTGHLRVLNREFIDAYENSSSEFIMLAKVKSTIEDIYRSQPDIGPYHKETVITAF 615

Query: 147 SEGSVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXXX--LPPRARSLKSFVVTSVVAFPTDSK 204
SEGSVIAYY SEF +P++ L PR R+ + V SVVAFP D
Sbjct: 616 SEGSVIAYYLSEFIVPKYREEKLDRAMADKQSLVQRLNPRLRN-PTLKVESVVAFPADPS 674

Query: 205 TVQRTQDNSCSFGLHARGVELMRFTTPGFDPSPYPAHARCQWALRGDADSVLSLTFRSFD 264
Q +DNSC F LHA+ E+ F TPGFP SPYP +ARC WALR DA+SV+SLTF++ D
Sbjct: 675 IAQTARDNSCLFALHAKEGEITSFNTPGFPHSPYPNNARCYWALRADANSVISLTFKTL D 734

Query: 265 LASCDERGSIDLVTVYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQNVLLITLITNTERRH 324
L C + SD V VY++LSP+EPHALV+LCG Y PSYNLTF SSQNV+L+ LITN E R+
Sbjct: 735 LEQCTD-SSDYVKVYDSLSPVEPHALVRLCGNYAPSYNLTFSSQNVMLVALITNKEGRY 793

Query: 325 PGFEATFFQLPRMSSCGRLRKAQGTFNSPYYPGHYPNIDCTWNIEVPNNQHVKVRFKF 384
PGF+A FFQLP+M +CGG LR GTF +PYYP HYPP DC WNIEVP+ ++VKVRF
Sbjct: 794 PGFKAFFQLPKMKACGGTLRGESGTFPTPYPAHYPPATDCVWNIEVPSTKNVKVRFM 853

Query: 385 FYLLEPGVPAGTCTPKDYVEINGEKYCGERSQFVVTSSNSKITVRFHSDQSYTDTGFLAEY 444
F++LEPGVP +C KDYV+IN +YCGERSQFVV S++N+I V+FHSD+SYTDTGF AEY
Sbjct: 854 FFFLEPGVPVSSCTKDYVQINSTRYCGERSQFVVASSTNRIAVQFHSRSDSYTDTGFSAEY 913

Query: 445 LSYDSSDPCPGQFTCRTCRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFKCKPL 504
LSYDSSDPCPG+F C TGRCI K +RCDGW DC D SDE +C+C QF C+N +CKP
Sbjct: 914 LSYDSSDPCPGKFACNTGRCIEKSMRCDGWLDVCGSDERSCTC-TDQQFRCQNGWCKPK 972

Query: 505 FWVCDVNDGCGDNSDEQGCSCPAQTFRCNSNGKCLSKSQQCNGKDDCGDGSDEASCPKV-- 562
FWVCD+VNDGCGDNSDE CSC +F+C+NGKC+ +Q+C+GKDDCGDGSDE +C K
Sbjct: 973 FWVCDNVNDGCGDNSDELQCSCANNSFKCNNGKCIPTQKCDGKDDCGDGSDEGTCSKAAQ 1032

Query: 563 NVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSGSDGSKDCDCGLRSFTRQARVVGTDAD 622
+ V C +TY+C NGLC+SK NPECDG++DC D SDE +C+CG RS+ +++R+VGG ++D
Sbjct: 1033 STVACKSYTYKCRNGLCISKQNPEDGQKDCEDNSDEDNCNCGTRSYIKSRIVGGQNSD 1092

Query: 623 EGEWPWQVSLHALGQGHICGASLISPWLVSAAHCYIDDRGFRYSIPTQWTAFLGLHDQS 682
GEWPWQVSLHA QGH+CGASLIS WLVSAAHC+++ +G RYSD + WTA+LGL +QS
Sbjct: 1093 VGEWPWQVSLHAKSQGHVCGASLISETWLVSAAHCFLQLGIRYSDASLWTAYLGLTNQS 1152

Query: 683 QRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAG 742
+R+ VQ +++KRIISH FND+T+DYDIA++EL+ P +S++V+PICLPD++H FP G
Sbjct: 1153 KRNDANVQMKQIKRIISHRSFNDYTYDYDIAVIELQSPVTFSAVVQICLPDSTHNFVPG 1212

Query: 743 KAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCCENLLPQQITPRMMCVGFLSGGVDSCQ 802
K +WVTGWG T GG+G+ ILQK EIRVINQ T C LL Q+T RMMCVG L+GGVD+CQ
Sbjct: 1213 KDLWVTGWGATVEGGSGSTILQKAEIRVINQTVCNRLTLDQLTERMMCVGVLTGGVDACQ 1272

Query: 803 GDSGGPLSSVEADGRIFQAGVVSWDGCAQRNKPVGYYTRLPLFRDWIKENTGV 855
GDSGGPL SVE GR+F AGVVSWDGCAQRNKPVGYY+RL R WIK+ TG+
Sbjct: 1273 GDSGGPLSVSVENSGRMFLAGVVSWDGCAQRNKPVGYSRLTALRTWIKQQTGL 1325

☐ >gi|49257232|gb|AAH71077.1| ☒ Stl4-A-prov protein [Xenopus laevis]
Length = 845

Score = 1008 bits (2607), Expect = 0.0

Identities = 459/840 (54%), Positives = 603/840 (71%), Gaps = 10/840 (1%)

```
Query: 22  YNSRHEKVNGLVEEVEFLPVNNVKKVEKHGPGRWXXXXXXXXXXXXXXXXXXXXXWHLQY 81
           YN+R + +NG EEGVEFLP N KKVEK GP + WH Y
Sbjct: 10  YNNRPQSLNGFEVEFLPATNSKKVEKTGPKKKLAIFGLVIGAALLSLTIGLLVWHFAY 69

Query: 82  RDVRVQKVFNQYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKES 141
           R+ V K++ GY+ I N F+DAYENS + EF L++KV D L+ +Y+G + PY ++
Sbjct: 70  RNKPVNKLTYGTLTIANTPFIDAYENSTTAEFSDLSAKVIDTLQTVYNGNKDIAPYLQKC 129

Query: 142  AVTAFSEG---SVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXXXLPPRARSLSFVVTSVVA 198
           +++AFSEG +VI YYWSEFS+P + PR R+ F + S+VA
Sbjct: 130  SISAFSEGGNNVIGYYWSEFSVPAFREAAFEKAISELKLPVNPQRQT---FALDSLVA 186

Query: 199  FPTDSKTVQRTQDNSCSFGLHARGVELMRFTTPGFDPSPYPAHARCQWALRGDADSVLSL 258
           +PTD + + +++SC++ LH+ + F++PGFDPSPYP +ARC W LR DA ++ L
Sbjct: 187  YPTDPQIARVFNSSCAYFLHSSNGVVAKFSSPGFDPSPYPRNARCLWTLRADAGRIHL 246

Query: 259  TFRSFDLASCDERGSDDLVTYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQNVLITLIT 318
           F++F + C G D V VY++LSP+EP A ++LCG YPPSYNLTF SS NV+L+TL+T
Sbjct: 247  HFKTFKMEKCKPNGGDFVMVYDSLSPIEPRAQIRLCGIYPPSYNLTFSSSNVMLVTLVT 306

Query: 319  NTERRHPGFEATFFQLPRMSSCGGLRKAQGTENSPPYPGHYPNIDCTWNIEVPNNQHV 378
           + + PGF A F QLP+ S CGG +R A G SPY+P HYPP+ +C W+I+VP+N+ V
Sbjct: 307  DNVGKFPGFLAEFKQLPKTSLCGGLIRDASGFITSPYFPAHYPPSTECIWDIQVDPNKEV 366

Query: 379  KVRFKFFYLLEPGVPAGTCTPKDYVEINGEKYCGERSQFVVTNSNKITVRFHSDQSYTDT 438
           KVRF FYL EPGVP C KD+VEI G+KYCGE+ FVV++NS+K++VRF SDQSYTDT
Sbjct: 367  KVRFNMFYLAEPGPVTKCTKDFVEIKGQKYCGEKEFFVVSNNSSKMSVRFVSDQSYTDT 426

Query: 439  GFLAEYLSYDSSDPCPGQFTCRTRGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKN 498
           GF AEYLSY+ +PCP QFTCR+GRCIR + +CDGW DC D SDE++C+C A QF C N
Sbjct: 427  GFTAELSYEPNPNCPDQFTCRSGRCIRLDQKCDGWNDCEDFSDEMSCTCTA-LQFRVCN 485

Query: 499  -KFCKPLFWVCDVNDGCDNSDEQGCSCPAQTFRCNSNGKCLSKSQQCNGKDDCGDGSDEA 557
           K CKP +++CD VNDGCD+SDE C CP TF+C NGKC+ SQ+C+ D+CGDGSDEA
Sbjct: 486  SKLCKPSYFICDGVNDGCDSSDELACKCPNNTFKCGNGKCIPDSQKCDRVDNCGDGSDEA 545

Query: 558  SCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSGDSDEK--DCDCGLRSFTRQARV 615
           C +V CT++TY+C N C++K NPECDG+ DCSDGSDE C+CG R FT+++R+
Sbjct: 546  ECDQVLTACTEYTYKCKNNQCITKKNPECDGENDCSGSDENAAKCNCGKRPFTKKSRI 605

Query: 616  VGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSPTQWTAF 675
           VGG +AD GE+PWQVSLHA G H CGASL+SP L+SAHC+ DD RYSD + WTA+
Sbjct: 606  VGGVNADTGEFPWQVSLHAKGNKHTCGASLVSPTMLISAHCQDDHQMRYSDASLWTAY 665

Query: 676  LGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDA 735
           LGLHDQ+Q + V ER++KRI++H FND T+D DIA+LELEKP EY+ ++P+C+P++
Sbjct: 666  LGLHDQAQLNTKDVVERKIKRIMAHIGFNDNTYDNDIAVLELEKPVEYTDIFIQVPCIPES 725

Query: 736  SHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCCENLLPQQITPRMCMCVGFLS 795
           +H FP GK IWVTGWG + GG A+ILQK EIR+INQT C LL Q+TPRM+C GF+S
Sbjct: 726  THDFPVGKPIWVTGWGALKEGGGAIVLQKAEIRIINQTECNKLLDGQLTPRMLCAGFVS 785
```

Query: 796 GGVDSQGDSSGGLSSVEADGRIFQAGVVSWDGCAQRNKPVGYYTRLPLFRDWIKENTGV 855
 GG+D+CQGDSSGGLSSVE + +++ AGVVSWG+GCA+RNKPGVYT++ + RDWIK+ TG+
 Sbjct: 786 GGIDACQGDSSGGLSSVELNNKVYLAGVVSWGEGCARRNKPVGYYTKVSMRDWIKDKTGL 845

☐ >gi|9757702|dbj|BAB08218.1| ☒ homolog of human MT-SP1 [Xenopus laevis]
 Length = 845

Score = 998 bits (2581), Expect = 0.0
 Identities = 457/840 (54%), Positives = 599/840 (71%), Gaps = 10/840 (1%)

Query: 22 YNSRHEKVNGLLEEGVEFLPVNNVKKVEKHGPGRWXXXXXXXXXXXXXXXXXXXXXWHLQY 81
 YN+R + +NG EEGVEFLP N KKVEK GP + WH Y
 Sbjct: 10 YNNRPQSLNGFEEGVEFLPATNSKKVEKTGPKKKLAIFGLVIGAALLSLTIGLLVWHFAY 69

Query: 82 RDVRVQKVFNQGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKES 141
 R+ V K++ GY+ I N F+DAYENS + EF L++KV D L+ +Y+G + PY ++
 Sbjct: 70 RNKPVNKLTYGTYLTIANTPFIDAYENSTTAEFSDLSAKVIDTLQTVYNGNKDIAPYLQKC 129

Query: 142 AVTAFSEG---SVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXXXXXLPPRARSILKSFVVTSVVA 198
 +++AFSEG +VI YYWSEFS+P + PR R+ F + S+VA
 Sbjct: 130 SISAFSEGGNNVIGYYWSEFSVPAFREAAFEKAISELKLPVSNPRQRT---FALDSLVA 186

Query: 199 FPTDSKTVQRTQDNSCSFGLHARGVELMRFTTGPFPDSPYPAHARCQWALRGDADSVLSL 258
 +PTD + + +++SC++ LH+ + +F++PGFPDSPYP +ARC W LR DA ++ L
 Sbjct: 187 YPTDPQIARVFNSSCAYFLHSSNGVVAKFSSPGFPDSPYPRNARCLWTLRADAGRIIHL 246

Query: 259 TFRSFDLASCDERGSDLVTYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQNVLITLIT 318
 F++F + C G D V VY++LSP+EP A ++LCG YPPSYNLTF SS NV+L+TL+T
 Sbjct: 247 HFKTFKMEKCKPNGGDFVMVYDSLSPIEPRAQIRLCGIYPPSYNLTFSSSNVMLVTLVT 306

Query: 319 NTERRHPGFEEATFFQLPRMSSCGRLRKAQGTFNSPYYPGHYPNIDCTWNIEVPNNQHV 378
 + + PGF A F QLP+ S CGG +R A G SPY+P HYPP+ + W+I+VP+N+ V
 Sbjct: 307 DNVGKFPGLAEFKQLPKTSLCGGLIRDASGFITSFYFPAHYPPSTESIWDIQVPDNKFV 366

Query: 379 KVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSNSNKITVRFHSDQSYTDT 438
 KVRF FYL EPGVP C KD+VEI G+KYCGE+ FVV++NS+K++VRF SDQSYTDT
 Sbjct: 367 KVRFNMFYLAEPGVPVTKCTKDFVEIKGQKYCGEKEFFVVSNNSSKMSVRFVSDQSYTDT 426

Query: 439 GFLAEYLSYDSSDPCPGQFTCRGTGRCIRKELRCDGWADCTDHSDELNCSDAGHQFTCKN 498
 GF AEYLSY+ +PCP QFTCR+GRCIR + +CDGW DC D SDE++C+C A QF C N
 Sbjct: 427 GFTAELYSEPRNPCPDQFTCRSGRCIRLDQKCDGWNDCEDFSDEMSCTCTA-LQFRCVN 485

Query: 499 -KFCKPLFWVCDVNDGCDNSDEQGCSCPAQTFRCNSNGKCLSKSQQCNGKDDCGDGSDEA 557
 K CKP +++CD VNDGCD+SDE C CP TF+C NGKC+ SQ+C+ D+CGDGSDEA
 Sbjct: 486 SKLCKPSYFICDGVNDGCDSSDELACKCPNNTFKCGNGKCI PDSQKCDRVDNCGDGSDEA 545

Query: 558 SCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEK--DCDCGLRSFTRQARV 615
 C +V CT++TY+C N C++K NPECDG+ DCSDGSDE C+CG R FT+++R+
 Sbjct: 546 ECDQVLTTACTEYTYKCKNNQCITKKNPECDGENDCSDGSDENAAKCNCGKRPFTTKSRI 605

Query: 616 VGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAF 675
 VGG +AD GE+PWQVSLHA G H CGASL P L+SAAHC+ DD RYSD + WTA+
 Sbjct: 606 VGGVNADTGEFPWQVSLHAKGNKHTCGASLGFPMTLISAACFQDDHQMRYSDASLWTAY 665

Query: 676 LGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMRPICLPDA 735
 LGLHDQ+Q + V ERR+KRI++H FND T+D DIA+LELEKP EY+ ++P+C+P++
 Sbjct: 666 LGLHDQAQLNTKDVVERRIKRIHAHIGFNDNTYDNDIAVLELEKPVETDFIQPVICIPES 725

Query: 736 SHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCEENLLPQQITPRMCMCVGFLS 795
 +H FP GK IWVTGWG + GG A+ILQK EIR+INQT C LL Q+TPRM+C GF+S
 Sbjct: 726 THDFPVGKPIWVTGWGALKEGGGAIVLQKAEIRIINQTECNKLLDGQLTPRMLCAGFVS 785

Query: 796 GGVDSCQGDSSGGLSSVEADGRIFQAGVVSWDGCAQRNKPVGVTPLPLFRDWIKENTGV 855
 GG+D+CQGDSSGGLSSVE + +++ AGVVSWG+GCA+RNKPGVYT++ + RDW K+ TG+
 Sbjct: 786 GGIDACQGDSSGGLSSVELNNKVYLAGVVSWECEGARRNKPVGVTKVSMRWDWSKDKTGL 845

☐ >gi|52354617|gb|AAH82854.1| Unknown (protein for MGC:81690) [Xenopus laevis]
 Length = 845

Score = 993 bits (2566), Expect = 0.0
 Identities = 450/840 (53%), Positives = 592/840 (70%), Gaps = 10/840 (1%)

Query: 22 YNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWXXXXXXXXXXXXXXXXXXXXXWHLQY 81
 YN++ + +NG EEGVEFLP N KKVEK GP + WH Y
 Sbjct: 10 YNNKPQSLNGFEEGVEFLPATNSKKVEKTGPKKKLAIFGVVIGAALISLTIGLLVWHFAY 69

Query: 82 RDVRVQKVFNQGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKES 141
 R+ + K++ GY+ I N F++AYENS + EF L++KV + L+ +Y+G + PY ++
 Sbjct: 70 RNAPIHKLYTGYLTIANQTFIEAYENSTTPEFADLSAKVINTLQTVYNGNKDIAPYLQQC 129

Query: 142 AVTAFSEGS---VIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXXXXXLPPRARSLKSFFVTSVVA 198
 +++AFSEG+ VI YYWSEFS+P + PR R+ F V S+VA
 Sbjct: 130 SISAFSEGNGNNVIGYYWSEFSVPAFREAAFEKAISEFKLPSVDPRRRT---FAVDSIVA 186

Query: 199 FPTDSKTVQRTQDNSSCFGLHARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSL 258
 + TD +T + +++SC++ LH+ + F++PGFPDSPYP +ARC W LR +A ++ L
 Sbjct: 187 YSTDPTQTRIFRNSCAYFLHSSDGAVAKFSSPGFPDSPYPRNARCLWTLRANAGQIIHL 246

Query: 259 TFRSFDLASCDESGDLVTVYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQNVLITLIT 318
 F++F + C G D V VY++LSPMEP A ++LCG YPPSYNLTF SS NV+L+TL+T
 Sbjct: 247 HFKTFKMECKINGGDFVMVYDLSLSPMEPRAQIRLCGIYPPSYNLTFSSSSNMLVTLVT 306

Query: 319 NTERRHPGFEEATFFQLPRMSSCGRLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHV 378
 + + PGF A F QLP+ S CGG +R A G SPY+P +YPP +C W+I+VP + V
 Sbjct: 307 DNVGKFPGLAEFRQLPKKSLCGGHIRDATGVITSPYFPAYYPPKTECIWDIQVPGKFFV 366

Query: 379 KVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERSQFVVTSSNSKITVRFHSDQSYTDT 438
 K+RF FYL EPGVP C KD+VEI G+KYCGER FVV++NS+KI+VRF SDQSY DT
 Sbjct: 367 KLRFNMFYLAEPGPVPTKCTKDFVEIEGQKYCGERKVFVVSNNSSKISVRFVSDQSYADT 426

Query: 439 GFLAEYLSYDSSDPCPGQFTCRGTGRCIRKELRCGDWADCTDHSDELNCSDAGHQFTCKN 498
 GF A+YLSY+ +PCP QFTC+TGRCIR + +CDGW DC D SDE C+C A QF C +
 Sbjct: 427 GFTADYLSYEPNPPCPDQFTCTGTGRCIRLDQKCDGWNDCEDFSDEKKCTCTA-QQFRCTD 485

Query: 499 -KFCKPLFWVCDVNDGCGNSDEQGCSCPAQTFRCSSNGKCLSKSQQCNGKDDCGDGSDEA 557
 K CKP +VCD VNDGCGNSDE C CP TF+C NGKC SQ+C+ D+CGDGSDEA
 Sbjct: 486 SKLCKPSHFVCDGVNDGCGNSDELSCKCPNSTFKCGNGKCFPDSQKCDRTDNCGDGSDEA 545

Query: 558 SCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSGDSDEKD--CDCGLRSFTRQARV 615
 C +V CT++TY+C N C++K NPECDG+ DC DGSDE C+CG R FT+++R+
 Sbjct: 546 DCGQVRTTVCTEYTYKCKNNQCITKKNPECDGENDCIDGSDENSAKCNCGKRPFTTKSRI 605

Query: 616 VGGTDADEGEWPQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFYSDPTQWTAF 675
 +GG +AD GE+PWQVSLH G H CGASL SP L+SAHC+ DD RYSD + WTA+
 Sbjct: 606 IGGVNADLGEFPWQVSLHVKGSKHTCGASLASPTTLISAHCQDDHSMRYSDASLWTAY 665

Query: 676 LGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDA 735
 LGLHDQ+Q + V ER++KRI++H FND T+D DIA+LELEKP +Y+ ++PIC+P++
 Sbjct: 666 LGLHDQAQLNTKNVVERKIKRIMAHIGFNDNTYDNDIAVLELEKPVDTDFIQPICIPES 725

Query: 736 SHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCCENLLPQQITPRMCMCVGFLS 795
 +H FP GK IWVTGWG + GG A+ILQK EIRVINQ T C LL Q+TPRM+C GF+S
 Sbjct: 726 THDFPVGKPIWVTGWGALKEGGGAIVLQKAEIRVINQTECNKLLDGLTPRMLCAGFVS 785

Query: 796 GGVDSQCQDGGPLSSVEADGRIFQAGVVSWDGCAQRNKPVGYYTRLPFRDWIKENTGV 855
 GG+D+CQDGGPLSSV+ + +++ AG+VSWG+GCA+RNKPGVYT++ + RDWIK+ TG+
 Sbjct: 786 GGIDACQDGGPLSSVDLNNKVYLAGIVSWGEGCARRNKPVGYYTKVSMRMDWIKDKTGL 845

☐ >gi|17390323|gb|AAH18146.1| ☒ ST14 protein [Homo sapiens]
 Length = 422

Score = 920 bits (2379), Expect = 0.0
 Identities = 422/422 (100%), Positives = 422/422 (100%)

Query: 434 SYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQ 493
 SYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQ
 Sbjct: 1 SYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQ 60

Query: 494 FTCKNKFCCKPLFWVCDVNDGCGNSDEQGCSCPAQTFRCNKGKLSKSKQCCNGKDDCGDG 553
 FTCKNKFCCKPLFWVCDVNDGCGNSDEQGCSCPAQTFRCNKGKLSKSKQCCNGKDDCGDG
 Sbjct: 61 FTCKNKFCCKPLFWVCDVNDGCGNSDEQGCSCPAQTFRCNKGKLSKSKQCCNGKDDCGDG 120

Query: 554 SDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSGDSDEKDCDCGLRSFTRQA 613
 SDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSGDSDEKDCDCGLRSFTRQA
 Sbjct: 121 SDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSGDSDEKDCDCGLRSFTRQA 180

Query: 614 RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSPTQWT 673
 RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSPTQWT
 Sbjct: 181 RVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSPTQWT 240

Query: 674 AFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLP 733
 AFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLP
 Sbjct: 241 AFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLP 300

Query: 734 DASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCCENLLPQQITPRMCMCVGF 793
 DASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCCENLLPQQITPRMCMCVGF
 Sbjct: 301 DASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCCENLLPQQITPRMCMCVGF 360

Query: 794 LSGGVDSQCQDGGPLSSVEADGRIFQAGVVSWDGCAQRNKPVGYYTRLPFRDWIKENT 853
 LSGGVDSQCQDGGPLSSVEADGRIFQAGVVSWDGCAQRNKPVGYYTRLPFRDWIKENT
 Sbjct: 361 LSGGVDSQCQDGGPLSSVEADGRIFQAGVVSWDGCAQRNKPVGYYTRLPFRDWIKENT 420

Query: 854 GV 855
 GV
 Sbjct: 421 GV 422

Score = 38.5 bits (88), Expect = 0.87
 Identities = 25/95 (26%), Positives = 34/95 (35%), Gaps = 26/95 (27%)

Query: 395 GTCPKDYVEINGEKYCGERSQFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCP 454
 G C + NG+ CG+ S N +T H+
 Sbjct: 102 GKCLSKSQCCNGKDDCGDGSDEASCPKVNVTCTKHT----- 138

Query: 455 GQFTCRTGRCIRK-ELRCDGWADCTDHSDELNCSC 488
+ C G C+ K CDG DC+D SDE +C C
Sbjct: 139 --YRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDC 171

☐ >gi|47225569|emb|CAG12052.1| unnamed protein product [Tetraodon nigroviridis]
Length = 730

Score = 740 bits (1911), Expect = 0.0
Identities = 363/741 (48%), Positives = 471/741 (63%), Gaps = 16/741 (2%)

Query: 120 VKDALKLLYSGVPFLGPYHKESAVTAFSEGSVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXX 179
V L Y FL YH +S VTAFSEG VIAYYWS+F IP H
Sbjct: 1 VSSQLGTTYKNDTFLSKYHTKSVVTAFSEG-VIAYYWSQFDIPVHDLEILPIFSEERVLS 59

Query: 180 XLPP---RARSLKSFVVTSVVAFPDTSKTVQRTQDNCSFGLHARGVELMRFTTPGFPDS 236
L R RS + V V V T + C F L A E M F++PG+P
Sbjct: 60 VLENNIVRTRSTQGSVRIREVTASCRDIWVAATGQDDCFFRLEAEEQEKM-FSSPGYPVK 118

Query: 237 PYPAHARCQWALRGDADSVLSLTFRSFDLASCDERGSDLVTYNTLSPMEPHALVQLCGT 296
YP +RCQW +R ++ +S++F F + D+ D V++Y++LSP + A+ + CG
Sbjct: 119 -YPPRSRCQWQIRASEENAI SVSFPFFHIE--DDCSDDFVSIYDSLSPDSSQAITEKCGQ 175

Query: 297 YPPSYNLTFHSSQNVLITLITNTERRHPGFEATFFQLPRMSS--CGGRLRKAQGTFNSP 354
PPS L SS N++LI LIT++E + PGF A + +P+ ++ CGG L G SP
Sbjct: 176 RPPSNPLEVTSSGNIMLINLITDSEVQQPGFLARYSAIPKSNATTCGGVLTADTGVITSP 235

Query: 355 YYPGHYPNIDCTWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCGERS 414
YP YPP +DC W I+VP ++V+++F F + EPGV C KD+VE+ G KYCGE
Sbjct: 236 LYPSSYPPAVDCKWTIKVPAGRNVRIKFTLFRMKEPGVDTRVCHKDFVEVMGTYKCGEIP 295

Query: 415 QFVVTSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGW 474
F +T+N N + V+FHSD SYTD GF AEY ++D S+PCP +F C +GRCI KELRCDGW
Sbjct: 296 YFTLTNTNENVLDVKFHSDGSYTDKGFSAEYSAFDPSNPCPNKFACNSGRICISKELRCDGW 355

Query: 475 ADCTDHSDELNCSCDAGHQFTCKNKFCCKPLFWVCDNVDCGDNDSDEQGCSCPAQTFRCNS 534
DC D SDE+ C C+ QF CKN CKP WVCD VNDCGD SDE CSC FRCS+
Sbjct: 356 NDCGDMSEMMQCCEKD-QFACKNGLCKPNLWVCDRVNDCGDWSDEAKSCSEKNEFRCSS 414

Query: 535 GKCLSKSQQCNGKDDCGDGSDEASCPKVNVTCTKH TYRCLNGLCLSKGNPECDGKEDCS 594
G CL + CN K DC DGSDEA+C + + TC++ TY C N +C++K N ECD DCS
Sbjct: 415 GLCLPQDVVCNQKRDVCDGSDEANC-ETSKGTCSEFTYMCKNQVCINKLNAECDRVNDCS 473

Query: 595 DGSDEKDCDCGLRSFTRQARVVGTDADGEWQPQVSLHALGQGHICGASLISPWLVS 654
D SDE C CG R + + R+VGG +A+ GEWQPQVSLH L GH+CGAS+IS WL+SA
Sbjct: 474 DSSDEAACGCGRPY-KLNRIVGGQNAEVGEWQPQVSLHFLTYGHVCGASIIISERWLLSA 532

Query: 655 AHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIAL 714
AHC++ + W + G+ DQ ++ G+ R LKRIISHP +N T+DYDIAL
Sbjct: 533 AHCFTVTSSPQNHI-AANWLTYSGMQDQYKQD--GILRRPLKRIISHPPDYNQMTYDYDIAL 589

Query: 715 LELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQT 774
LEL +P E+++ ++PICLPD+SH+FPAG + WVTGWG + GG A +LQK +++IN T
Sbjct: 590 LELSEPLEFTNTIQPICLPDSSHMFPAGMSCWVTGWGAMREGGQKAQLLQKASVKIINGT 649

Query: 775 TCENLLPQQITPRMMCVGFLSGGVDSCQGDSSGGLSSVEADGRIFQAGVSWGDGCAQRN 834
C + Q+T RM+C GFL+GGVD+CQGDSSGGL E G+ FQAG+VSWG+GCA+RN
Sbjct: 650 VCNEVTEGQVTSRMLCSGFLAGGVDACQGDSSGGLVCFEESGKWFQAGIVSWGEGCARRN 709

Query: 835 KPGVYTRLPLFRDWIKENTGV 855
KPG+YTR+ R WIKE G+
Sbjct: 710 KPGIYTRVTKLRKWIKEQIGI 730

☐ >gi|10179932|gb|AAG13949.1| **G** serine protease SNC19 [Homo sapiens]
Length = 325

Score = 727 bits (1876), Expect = 0.0
Identities = 325/325 (100%), Positives = 325/325 (100%)

Query: 340 CGGRLRKAQGTFNSPYYPGHYPNIDCTWNIEVPNNQHVKVRKFFYLLEPGVPAGTCPK 399
CGGRLRKAQGTFNSPYYPGHYPNIDCTWNIEVPNNQHVKVRKFFYLLEPGVPAGTCPK
Sbjct: 1 CGGRLRKAQGTFNSPYYPGHYPNIDCTWNIEVPNNQHVKVRKFFYLLEPGVPAGTCPK 60

Query: 400 DYVEINGEKYCGERSQFVVTNSNKitVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTC 459
DYVEINGEKYCGERSQFVVTNSNKitVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTC
Sbjct: 61 DYVEINGEKYCGERSQFVVTNSNKitVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTC 120

Query: 460 RTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCCKPLFWVCDVND CGDNSD 519
RTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCCKPLFWVCDVND CGDNSD
Sbjct: 121 RTGRCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFCCKPLFWVCDVND CGDNSD 180

Query: 520 EQGCSCPAQTFRC SNGKCLS KSKSQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLC 579
EQGCSCPAQTFRC SNGKCLS KSKSQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLC
Sbjct: 181 EQGCSCPAQTFRC SNGKCLS KSKSQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLC 240

Query: 580 LSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGTTDADEGEWPWQVSLHALGQGH 639
LSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGTTDADEGEWPWQVSLHALGQGH
Sbjct: 241 LSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGTTDADEGEWPWQVSLHALGQGH 300

Query: 640 ICGASLISP NWLVSAAH CYIDDRGF 664
ICGASLISP NWLVSAAH CYIDDRGF
Sbjct: 301 ICGASLISP NWLVSAAH CYIDDRGF 325

☐ >gi|47227882|emb|CAG09045.1| unnamed protein product [Tetraodon nigroviridis]
Length = 910

Score = 702 bits (1811), Expect = 0.0
Identities = 363/827 (43%), Positives = 482/827 (58%), Gaps = 61/827 (7%)

Query: 33 EEGVEFLPVNNVKKVEKH-GPGRWXXXXXXXXXXXXXXXXXXXXXWHLQYR-DVRVQKVF 90
E V+FLP ++ K+EK GPG+ WH ++R D+RV+KV+
Sbjct: 1 ESSVQFLPASDNTKLEKKKPGKGTGAVIGVVILAVVVALMIGLLVWHFRFRQDIRVKKVY 60

Query: 91 NGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKESAVTAFSEGS 150
G MRITN+ F +AYE+SN+TEF +LA +V LK +YS P L Y+ S V AFSEGS
Sbjct: 61 TGSMRITNQVFENAYEDSNTTEFKALAKQVVTQLKTIYSKSPQLAKYYVGSTVQAFSEGS 120

Query: 151 VIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXLPPRA---RSLKSFVVTSVVAFPTD----- 202
V+AYY SEF +P + R+ S + +VV+ D
Sbjct: 121 VVAYYLSEFRVPVGQEAAVDKAMAAMEQLVNKEQRSVYRAGNSLMFDNVVSSALDTRMTS 180

Query: 203 -----SKTVQRTQDNCSFGLHARGVELMRFTTPGFDPSPYPAHARCQWALRGDA 252
S + + S F HA+ + + +PGFP+ PY + QW LR D

Sbjct: 181 ASFSRSPELNSNVIVDSASGSLQFSEHAKPNYIGQIQSPGFNHPYSPNTLVQWRLRADP 240

Query: 253 DSVLSLTFRSFDLASCDEGRSDLVTVYNTLSPMEPHALVQLCGTYPPSYNLTFFHSSQNVL 312
D V+ L F + +L + +D + +Y++L +E + +LCG + PS +TF SS NVL

Sbjct: 241 DYVIQLKFDTINLEN--NCTNDFIRIYDSLVSIESRIMDEL CGYHSPSEPMTFISSGNVL 298

Query: 313 LITLITNTERRHPGFEATFFQLPRMSS---CGGRLRKAQGTFNSPYYPGHYPNIDCTWN 369
L+ + TN + +PGF A Q+ R S CGG+L G F SP +P +YP I C W

Sbjct: 299 LVAMATNDMKNYPGFRAQVSQVKRGSPATVCGGKLSGENGKFTSPNFPNYYPARISCQWT 358

Query: 370 IEVPNNQHVKVRFKFFYLLEPGVP-AGTCPKDYVEINGEKYCGERSQFVVT--SNSNKIT 426
I+VP + VKV+F+ F L EPG CPKDYV+ING+K CGE+ + VT S++N +

Sbjct: 359 IQVPAGKVVKVFRKFLLEPGQERVKNCPKDYVQINGKKVCGEQPDWAVTETSSTNTMD 418

Query: 427 VRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDHSDELNC 486
V F SD S+ D GF AE+ + D+ + CP +F CR RCI+ EL+CDGW DC D SDE+NC

Sbjct: 419 VLFVSDSSHVDRGFEEFQAVDADNLCPNKFQCRNQRCIKSELQCDGWNDCCGMSDEVNC 478

Query: 487 SCDAGH-----QFTCKNKFKPLFWVCDSVNDCCG 516
S H TCKN CKP+FW CD V+DCGD

Sbjct: 479 SERRSHTRPIVRNPSKMKHSFKIHSPKFCSPECNSKDITCKNGLCKPMFWKCDGVDDCGD 538

Query: 517 NSDEQGCS-CPAQTFRCSNGKCLSKSQCCNGKDDCGDGSDEASCPKVNVTCTKHTYRCL 575
+DEQ C CP F+C N KC+S+ QC+ +DDCGDGSDE +C + CT TYRC

Sbjct: 539 KTDEQNCGDCPTGQFKCQNKKCISEKNQCDSDCGDGSDEINCGRNTDAKCTDLTYRCS 598

Query: 576 NGLCLSKGNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVGGTDADEGEWPWQVSLHAL 635
N C++K NPECDG DC DGSDE +C CG F R +R+VGG ADEGE+PWQVSLH

Sbjct: 599 NNNKICITKVNPECDGTPDCEDGSDEVNCGCGKNVF-RTSRIVGGEVADEGEFPWQVSLHIK 657

Query: 636 GQGHICGASLISPNWLVSAAHCYIDDRGFYSPTQWTAFLGLHDQSQRSAPGVQERRLK 695
+GH+CGAS+ISPNWLVA+AAHC D+ R S P W A+LGLH Q Q V R LK

Sbjct: 658 NRGHVCGASIIISPNWLVTAAHCVDQDEGTLRLSQPGSWEAYLGLHVQ-QNIKKSVVVRNLK 716

Query: 696 RIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQY 755
RII HP +N++T+D D+AL+EL+ P YS ++PICLP H FP G+ +W+TGWG T+

Sbjct: 717 RIIPHPNYNEYTYDNDVALMELDSPVTYSYDIQPICLPAPQHDFPVGETVWITGWGATRE 776

Query: 756 GGTGALILQKGEIRVINQTTCCENLLPQQITPRMMC VGFLSGGVDSCQ 802
G A +LQK ++R+INQ TC +L+ QIT RM+C G L+GGVD+CQ

Sbjct: 777 EGPAATVLQKAQVRIINQDTCNSLMGGQITSRMLCAGVLTGGVDACQ 823

☐ >gi|49900216|gb|AAH76994.1| ☒ MGC89623 protein [Xenopus tropicalis]
gi|52346064|ref|NP_001005075.1| ☒ MGC89623 protein [Xenopus tropicalis]
Length = 663

Score = 690 bits (1781), Expect = 0.0
Identities = 317/609 (52%), Positives = 417/609 (68%), Gaps = 10/609 (1%)

Query: 22 YNSRHEKVNGLEEGVEFLPVNNVKKVEKHGPGRWXXXXXXXXXXXXXXXXXXXXXWHLQY 81
YN+R + +NG EEGVEFLP N KKVEK GP + WH Y

Sbjct: 10 YNNRPQSMNGFEEGVEFLPAANTKKVEKAGPKKKLAIFGVVIGAALLSLTIGLLVWHFAY 69

Query: 82 RDVRVQKVFNMGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKES 141
R+ VQK++ GY+RI N FV+AYENS + EF L+ KV L+ LY+G + PY ++

Sbjct: 70 RNAPVQKLYTGYLRIANTQFVEAYENSTTREFADLSVKVISTLRTLYNGEKDIAPYLQQC 129

Query: 142 AVTAFSEGS---VIAYYWSEFSI PQHLXXXXXXXXXXXXXXXXXLP PRARSLKSFVVTSVVA 198
 +++AFSEGS V+ YYWSEFS+P LP ++F V S+VA
 Sbjct: 130 SISAFSEGS DNNVGYWSEFSVP---AFREEAFEKAISELKLPTVNLQRFAVDSLVA 186

Query: 199 FPTDSKTVQRTQDNCSFGLHARGVELMRFTTPGFPD SPYPAHARCQWALRGDADSVLSL 258
 +PTD + + +++SC+F LH+ + +F++PGFPD+PYP +ARC W LR DA ++ L
 Sbjct: 187 YPTDPQIARNFKNSSCAFFLHSSAGVMTKFSSPGFPDTPYPPNARCLWTLRADAGQMIRL 246

Query: 259 TFRSFDLASCDERGS DLTVTYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQNVLITLIT 318
 F++F + C D V VY++LSP+EP A ++LCG YPPSYNLTF SS NV+L+TL+T
 Sbjct: 247 KFKTFKMEKCKANAGDFVMVYDSLPIEPRAQIRLCGIYPPSYNLTFSSSNVMLVTLVT 306

Query: 319 NTERRHPGFEATFFQLPRMSSCGGRLRKAQGTFN SPYYPGHYPNIDCTWNIEVPNNQHV 378
 + + PGF A F Q P+ S CGG +R A G F SPY+PGHYPP I+C W+I+VP+N+ V
 Sbjct: 307 DNVGKFPGLAEFSQFPKTS LCGGYIRDASGVFTSPYFPGHYPPKIECIWDIQVDPDNKFV 366

Query: 379 KVRFKFFYLLEPGVPAGTCKPKDYVEINGEKYCGERSQFVVTSSNSKITVRFHSDQSYTDT 438
 K+RF FYL EPGVP C KD+VEING+KYCGER FVV++NS+K++VRF SDQSYTDT
 Sbjct: 367 KLRFMFYLAEPGVPTKCTKDFVEINGQKYCGERKFFVVSNNSSKMSVRFVSDQSYTDT 426

Query: 439 GFLAEYLSYDSSDPCPGQFTCRGTGR CIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKN 498
 GF AEYLSY+ +PCP QF C++GRCIR + +CDGW DC D SDE +C+C A QF C N
 Sbjct: 427 GFTAELSYEPNPNCPDQFACKSGRCIRLDQKCDGWNDCEDFSDEKSCTCTA-LQFRCTN 485





Query: 499 -KFKPLFWVCD SVNDCGDSDEQGCSCPAQTFRCSNGKCLSKSQQCNGKDDCGDGSDEA 557
 K CKP ++VCD VNDCGD+SDE C CP T++C NGKC+ +SQ+C+ D+CGDGSDEA
 Sbjct: 486 SKLCKPSYFVCDGVNDCGDSDELACQCPNNTYKCGNGKCI PESQKCDRTDNCGDGSDEA 545

Query: 558 SCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDE--KDCDCGLRSFTRQARV 615
 C +V TCT++TY+C N C++K NPECDG+ DCSDGSDE C+CG R FT+++R+
 Sbjct: 546 ECGRVLTTTCTEYTYKCKNNQCITKKNPECDGENDCSDGSDEISAKCNCGRPFTHKSRI 605

Query: 616 VGGTDADEG 624
 VGG +AD G
 Sbjct: 606 VGGVNADSG 614

Score = 87.0 bits (214), Expect = 2e-15
 Identities = 37/60 (61%), Positives = 51/60 (85%), Gaps = 3/60 (5%)

Query: 796 GGVDSQCQDGGPLSSVEADGRIFQAGVSWGDGCAQRNKP GYTR LPLFRDWIKENTGV 855
 GGV++ DSGGPLSSVE + +++ AG+VSWG+GCA+RNKP GYTR+ + RDWI++ TG+
 Sbjct: 607 GGVNA---DSGGPLSSVELNNKVYLAGIVSWGEGCARRNKP GYTRVAMMRDWIRDKTGL 663

 >[gi|18655574|pdb|1EAX|A](http://www.rcsb.org/pdb/entry/1EAX)  Chain A, Crystal Structure Of Mtspl (Matriptase)
[gi|18655572|pdb|1EAW|C](http://www.rcsb.org/pdb/entry/1EAW/C)  Chain C, Crystal Structure Of The Mtspl (Matriptase)-Bpt
 (Aprotinin) Complex
[gi|18655570|pdb|1EAW|A](http://www.rcsb.org/pdb/entry/1EAW/A)  Chain A, Crystal Structure Of The Mtspl (Matriptase)-Bpt
 (Aprotinin) Complex
 Length = 241

Score = 512 bits (1319), Expect = e-143
 Identities = 241/241 (100%), Positives = 241/241 (100%)

Query: 615 VVGGTDADEGEWPWQVSLHALGQGHICGASLISP NWLVSAAH CYIDDRGFRYSDPTQWTA 674
 VVGGTDADEGEWPWQVSLHALGQGHICGASLISP NWLVSAAH CYIDDRGFRYSDPTQWTA

Sbjct: 1 VVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSIPTQWTA 60

Query: 675 FLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPD 734
 FLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPD

Sbjct: 61 FLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPD 120

Query: 735 ASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTTCENLLPQQITPRMCMVGFL 794
 ASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTTCENLLPQQITPRMCMVGFL

Sbjct: 121 ASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTTCENLLPQQITPRMCMVGFL 180

Query: 795 SGGVDSCQGDSSGGLSSVEADGRIFQAGVSWGDGCAQRNKPVGYYTRLPLFRDWIKENTG 854
 SGGVDSCQGDSSGGLSSVEADGRIFQAGVSWGDGCAQRNKPVGYYTRLPLFRDWIKENTG

Sbjct: 181 SGGVDSCQGDSSGGLSSVEADGRIFQAGVSWGDGCAQRNKPVGYYTRLPLFRDWIKENTG 240

Query: 855 V 855
 V

Sbjct: 241 V 241

☐ >gi|47209610|emb|CAF89594.1| unnamed protein product [Tetraodon nigroviridis]
 Length = 435

Score = 453 bits (1166), Expect = e-126
 Identities = 210/424 (49%), Positives = 269/424 (63%), Gaps = 28/424 (6%)

Query: 453 CPGQFTCRTGRCIRKELRCDGWADCTDHSDELNC-----SCD 489
 CPG F C C+ LRCDW DC D+SDE +C CD

Sbjct: 14 CPGSFWCHNNLCLNPALRCDGWDDCGDNSDERDCRESTPALAPVTTCTDGAFLFLSAECD 73

Query: 490 AGHQFTCKNKFKPLFWVCDVNDGCGNSDEQGC-SCPAQTFRCNSNGKCLSKSQQCNGKD 548
 A Q C+N CKP FW CD +DCGNSDE C C F C N +C+ +S++C+G+D

Sbjct: 74 AS-QLRCQNGRCKPKFWQCDGTDDCGNSDEDNCVKCKPGEFLCRNQRCVPESRRCDGRD 132

Query: 549 DCGDGSDEASCPK-VNVVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGLR 607
 DC DGSDE+ C + V + C++H++RC NG C+SK NP+CDG+ DC D SDE C CG R

Sbjct: 133 DCSGDSDESQCKRSVLLQQCSEHSFRCRNGKCISKLPDCDGELEDCEDEDGCHCGKR 192

Query: 608 SFTRQARVVGTTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYS 667
 + R +R+VGG + E EWPWQVSLH G GH CGAS++S WL++AAHC + YS

Sbjct: 193 PY-RSSRIVGGQVSQEAEPWQVSLHIKGTGHTCGASVLSNRWLLTAHCVRNPGSAMYS 251

Query: 668 DPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMV 727
 P QW LGLH+Q Q S V+ R +K+II H ++ T+D DIAL+EL+ + +

Sbjct: 252 QPEQWEVLLGLHEQGQTSKWTVK-RSVKQIIPHRYDPVTYDNDIALMELDANVTNLQNI 310

Query: 728 RPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTTCENLLPQQITPR 787
 PICLP ++ FP G W+TGWG T+ GG A +LQK +R+IN T C +L+ ++T

Sbjct: 311 YPICLPSPITYYFPVGSEAWITGWGATREGGRPASVLQKAAVRIINSTVCRSLMSDEVTEG 370

Query: 788 MMCVGFLSGGVDSCQGDSSGGLSSVEADGRIFQAGVSWGDGCAQRNKPVGYYTRLPLFRD 847
 M+C G L GGVD+CQGDSSGGLS GR+F AGVSWGDGCA+RNKPVGYYTR +R

Sbjct: 371 MLCAGLLRGGVDACQGDSSGGLSFTSPSGRVFLAGVSWGDGCARRNKPVGYYTRTTQYRS 430

Query: 848 WIKE 851
 WI+E

Sbjct: 431 WIRE 434

☐ >gi|57086055|ref|XP_546396.1| PREDICTED: similar to matriptase [Canis familiaris]
Length = 2045

Score = 436 bits (1120), Expect = e-120
Identities = 204/247 (82%), Positives = 224/247 (90%), Gaps = 3/247 (1%)

Query: 212 NSCSFGLHARGVELMRFTTPGFPDSPYPAHARCQWALRGDADSVLSLTFRSFDLASCDER 271
+SCSF L HAR ELMRFTTPGFPDSPYPA ARCQW LRGDAD VLSLTFRSFD+A+CD+R
Sbjct: 993 DSCSFALHARS GELMRFTTPGFPDSPYPARARCQWTLRGDADFVLSLTFRSFDVATCDDR 1052

Query: 272 GSDLVTVYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQNVLLITLITNTERRHPGFEATF 331
GSDLV VY+TLSP+EP A+VQLCGTYPPSYNLTF SSQNVLL+TLITNTERRHPGFEATF
Sbjct: 1053 GSDLVMVYDTLSPVEPRAVQLCGTYPPSYNLTF LSSQNVLLVTLITNTERRHPGFEATF 1112

Query: 332 FQLPRMSSCGGRLRKAQGTFNSPYYPGHYPPNIDCTWNIEVPNNQHV KVRFKFFYLLEPG 391
FQLP++SSCGG LR +QGTf+SPYYPGHYPPN++CTW+IEVP++Q+VKV FK FY+LEP
Sbjct: 1113 FQLPKLSSCGGSLRGSQGTfSSPYYPGHYPPNMCTWDIEVPSHQNVKVLKAFYMLEPN 1172

Query: 392 VPAGTCPKDYVEINGEKYCGERSQFVVTSSNKNITVRFHSDQSYTDTGFLAEYLSYDSSD 451
P GTC KDYVE+NGEKYCGER QFVVTSSNKNITVRFHSDQSYTDTGFLAEYLSYDSSD
Sbjct: 1173 TPLGTCSKDYVEVNGEKYCGERPQFVVTSSNKNITVRFHSDQSYTDTGFLAEYLSYDSSD 1232

Query: 452 ---PCPG 455
P PG
Sbjct: 1233 REYPSPG 1239

Score = 424 bits (1090), Expect = e-117
Identities = 181/213 (84%), Positives = 196/213 (92%)

Query: 453 CPGQFTCRTCIRKELRCDGWADCTDHSDELNCSCDAGHQFTCKNKFKCKPLFWVCD SVN 512
CPG+F C TGRCIR ELRCDGWADCTD+SDELNC C+A +QFTCKNKFKCKPLFWVCD SVN
Sbjct: 1448 CPGKFMCHTGR CIRNELRCDGWADCTDYSDELNCQC NATYQFTCKNKFKCKPLFWVCD SVN 1507

Query: 513 DCGDNSDEQGCSCPAQTFRC SNGKCLSKSQQCNGKDDCGDGSDEASCPKVNVTCTKHTY 572
DCGDNSDEQ CSCPAQTFRC NGKCL ++QQC+G D+CGDGSDEA+C V V CTKHTY
Sbjct: 1508 DCGDNSDEQECSCPAQTFRCGNGKCLPQNQQCDGTDCG DGSDEATCDLVRTVACTKHTY 1567

Query: 573 RCLNGLCLSKGNPECDGKEDCS DGSDEKDCDCGLRSFTRQARVVGTTDADEGEWPQVSL 632
RC NGLCLSK NPECDGK+DCSDGSDEKDCDCGLRSFTRQ+RVVGGT+ADEGEWPQVSL
Sbjct: 1568 RCHNGLCLSKSNPECDGKKDCSDGSDEKDCDCGLRSFTRQSRVVGTTNADEGEWPQVSL 1627

Query: 633 HALGQGHICGASLISPNWLVSAAHCYIDDRGFR 665
H LGQGH+CGAS+ISPNWLVSAAHC+IDDRGFR
Sbjct: 1628 HVLGQGHVCGASIISPNWLVSAAHCFIDDRGFR 1660

Score = 127 bits (319), Expect = 1e-27
Identities = 66/99 (66%), Positives = 71/99 (71%), Gaps = 14/99 (14%)

Query: 757 GTGALILQKGEIRVINQTT CENLLPQQITPRMCMVGFLSGGVDSCQGD SGGPLSSVEADG 816
G+GAL+LQKGEIRVINQTT L GDSGGPLSSVEADG
Sbjct: 1961 GSGALVLQKGEIRVINQTTWRPALAADHAAH-----DGDSGGPLSSVEADG 2006

Query: 817 RIFQAGVVS WGDGCAQRNKPGVYTRLPLFRDWIKENTGV 855
RIFQAGVVS WGDGCAQR+KPGVYTRL +FRDWI+E TGV
Sbjct: 2007 RIFQAGVVS WGDGCAQRDKPGVYTRLAVFRDWIREETGV 2045

Score = 122 bits (307), Expect = 3e-26
Identities = 56/96 (58%), Positives = 70/96 (72%)

Query: 29 VNGLEEGVEFLPVNNVKKVEKHGPGRWXXXXXXXXXXXXXXXXXXXXXWHLQYRDVRVQK 88
++G+EEGVEFLPVNN +KVEK GP RW WH QY+++RVQK
Sbjct: 536 MSGVEEGVEFLPVNNTRKVEKRGPKRWVLLVTGLAGLVLLSLVACLLMWHFQYQNMVRVQK 595

Query: 89 VFNGYMRITNENFVDAYENSNSTEFVSLASKVKDAL 124
+FNGY+RITNENFVDAYENSNSTEF +LA++VK+A+
Sbjct: 596 IFNGYLRLITNENFVDAYENSNSTEFANLANRVKEAV 631

Score = 70.5 bits (171), Expect = 2e-10
Identities = 36/64 (56%), Positives = 42/64 (65%)

Query: 136 PYHKESAVTAFSEGSVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXXXXXLPPRARSLKSFVVT 195
P H ++ + SEGSVIAYYWSEFSIPQ+L LPPRAR+L SFV+TS
Sbjct: 792 PSHAPASRLSPSEGSVIAYYWSEFSIPQYLVEDAERVMAQERAAVLPPRARALNSFVLTS 851

Query: 196 VVAF 199
VVAF
Sbjct: 852 VVAF 855

Score = 44.3 bits (103), Expect = 0.016
Identities = 20/23 (86%), Positives = 21/23 (91%)

Query: 124 LKLLYSGVPFLGPHYHKESAVTAF 146
LKLLYSGVP LGPHYHK+S VTAF
Sbjct: 694 LKLLYSGVPSLGPYHKKSMVTAF 716

☐ >[gi|56417706|emb|CAI19335.1|](#) OTTHUMP00000028798 [Homo sapiens]
Length = 788

Score = 398 bits (1022), Expect = e-109
Identities = 251/786 (31%), Positives = 375/786 (47%), Gaps = 89/786 (11%)

Query: 83 DVRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKVKDAL KLLYSGVPFLGPHYKESA 142
+V V +V++G +R+ N +F S+ F S +K + LK L + LG Y+ S+
Sbjct: 72 EVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTR-LGTYYNSSS 130

Query: 143 VTAFSEGSVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXXXXXLPPRARSLKSFVVT SVVAFPTD 202
V +F EG + ++W IP+H L P +++ +V +++
Sbjct: 131 VYSFGEGLTCTFFWFILQIPEH-----RRLMLSPEV--VQALLVEELLSTVNS 176

Query: 203 SKTVQ-RTQDNCSFGLHARGVELMRFTTPGFP---DSPYPAHARCQWALRGDADSVLSL 258
S V R + GL G + G P + C W L+G D +L L
Sbjct: 177 SAAVPYRAEYEVDP EGLVILGCYRYSYVGQGVRLKGPDLHLASSCLWHLQGP KDLMLKL 236

Query: 259 TFRSFDLASCDERGS DLT VYNTLSPMEPHALVQLCGTYPPSYNLT FHSSQNVLITLIT 318
+ LA C +R + +Y+ P+E + + G + +S ++ +
Sbjct: 237 RLE-WTLAECRDR----LAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKK 291

Query: 319 NTERRHPGF----EATFFQLPRMSSCGGRLRKAQGTFN SPYYPGHYPNIDCTWNIEVPN 374


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      + F + FQ ++ +QG ++PY+P +Y P C+W++ VP+
Sbjct: 292 GLHSYYDPFVLSVQPVVFQACEVNLTLNRLDSQGVLSPTYFPSYISPQTHCSWHLTVPS 351

Query: 375 NQHVKVRFKFFYLLEPGVPAGTCPKDYVEINGEKYCG-----ERSQFVVTNSNSKIT 426
      + + Y L C + I + CG ER V T+ IT
Sbjct: 352 LDYGLALWFDAYALRRQKYDLPCQTQGWTIQNRRLCGLRILQPYAERIPVVATAG---IT 408

Query: 427 VRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDHSDELNC 486
      + F S S T G Y Y+ SDPCPG+F C
Sbjct: 409 INFTSQISLTGPGVRVHYGLYNQSDPCPGEF LCSV----- 443

Query: 487 SCDAGHQFTCKNKFCCKPLFWVCDSVND CGDNSDEQGCSCPAQTFRC S-NGKCLS KSKSQCN 545
      N C P CD V DC + DE+ C C A TF+C + C+S + C+
Sbjct: 444 -----NGLCVP---ACDGVKDCPNGLDERNCVCRA-TFQCKEDSTCISLPKVCD 488

Query: 546 GKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCG 605
      G+ DC +GSDE C + V C T++C + C+ K NP+CDG+ DC DGSDE+ CDCG
Sbjct: 489 GQPDCLNGSDEEQCEG--VPCGTFTTQCEDRSCVKKPNPQCDGRPDCRDGSD EHCDCG 546

Query: 606 LRSFTRQARVVG GTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFR 665
      L+ +R+VGG + EGEWPWQ SL G+ HICG +LI+ W+++AAHC+ +D
Sbjct: 547 LQG--PSSRIVGGAVSSEGEWPWQASLQVRGR-HICGGALIADRWVITAAHCFQEDS--- 600

Query: 666 YSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSS 725
      + WT FLG Q+ R PG ++ R++ HP+ + + DYD+ALL+L+ P S+
Sbjct: 601 MASTVLWTVFLGKVWQNSRW-PGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSA 659

Query: 726 MVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCE NLLPQQIT 785
      VRP+CLP SH F G W+TGWG + GG + LQK ++++I Q C + Q+T
Sbjct: 660 AVRPVCLPARSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEVYRYQVT 719

Query: 786 PRMCMVGFLSGGVDSQCQDSSGGPLSSVEADGRIFQAGVVS WGDGCAQRNKP G VYTRLPLF 845
      PRM+C G+ G D+CQGDSSGGL GR F AG+VSWG GC + N G VYTR+
Sbjct: 720 PRMLCAGYRKGKKDACQGDSSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGV 779

Query: 846 RDWIK E 851
      WI++
Sbjct: 780 ISWIIQ 785

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☐ >gi|34784418|gb|AAH57674.1| ☒ Tmprss6 protein [Mus musculus]
Length = 799

Score = 397 bits (1020), Expect = e-109

Identities = 247/785 (31%), Positives = 378/785 (48%), Gaps = 75/785 (9%)

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Query: 83 DVRVQKVFN GYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKESA 142
      +V V +V++G +R+ N +F S F S ++K + L+ L + LG Y+ S+
Sbjct: 71 EVTVSQVYSGSLRVLNRHFSQDLGRRESIAFRSESAKAQKMLQELVASTR-LGTYYNSSS 129

Query: 143 VTAFSEGSVIAIYWSEFSIPQH LXXXXXXXXXXXXXXXXXLP PRARSLKSFVVTSVVAFPTD 202
      V +F EG + ++W IP++ L S S + + + D
Sbjct: 130 VYSFGEGPLTCFFWFILDIPEY---QRLTSLPEVVRELLVDELLSNSSTLAS YKTEYEVD 186


Query: 203 SK--TVQRTQDN SCSFGLHARGVELMRFTTPG--FP-DSPYPAHARCQWALRGDADSVLS 257
      + + N G + PG P P C W L+G D ++
Sbjct: 187 PEGLVILEASVNDIVVLNSTLGCYRYSYVNP GQVLP LKGPDQQTTSCLWHLQGPEDLMIK 246

Query: 258 LTFRSFDLASC DERGSDLVTYNTLS PMEPHALVQLCGTYPPSYNLTFHSSQNVLLITLI 317

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+ + C +R V +Y+ P+E + + G + +S +V+ +
 Sbjct: 247 VRLE-WTRVDCRDR----VAMYDAAGPLEKRLITSVYGCSRQEPVMEVLASGSVMAVWVK 301
 Query: 318 TNTERRHPGF----EATFFQLPRMS-SCGGRLRKAQGTFNSPYYPGHYPPNIDCTWNIEV 372
 + F ++ FQ +++ + GRL QG +PYYP +Y P+ C+W++ V
 Sbjct: 302 KGMHSYDPPFLSVKSVAFQDCQVNLTLLEGRL-DTQGFLRTPYYPSPYSPSTHCSWHLTV 360
 Query: 373 PNNQHVKVRFKFFYLLEPGVPAGTCKPDYVEINGEKYCGERS-----QFVVTNSNKNITV 427
 P+ + + Y L C + I + CG R+ + + S+ +T+
 Sbjct: 361 PSLDYGLALWFDAYALRRQKYNRLCTQGQWMIQNRRLCGFRTLQPYAERI PMVASDGVTI 420
 Query: 428 RFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTCIRKELRCDGWADCTDHSDELNCS 487
 F S S T G Y Y+ SDPCPG+F C
 Sbjct: 421 NFTSQISLTGPGVQVYYSLYNQSDPCPGFELCSV----- 454
 Query: 488 CDAGHQFTCKNKFCKPLFWVCDSDVNDGDNDEQGCSCPAQTFRCSS-NGKCLSKSQQCNG 546
 N C P CD + DC + DE+ C C A F+C + C+S + C+
 Sbjct: 455 -----NGLCVP---ACDGIKDCPNGLDERNCVCRAM-FQCQEDSTCISLPRVCDR 500
 Query: 547 KDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGL 606
 + DC +GSDE C + V C T++C + C+ K NPECDG+ DC DGSDE+ CDCGL
 Sbjct: 501 QPDCLNGSDEEQCQEG--VPCGTFTFQCEDRSCVKKPNPECDGQSDCRDGSDEQHCDCGL 558
 Query: 607 RSFTRQARVVGTTDADEGEWPWQVSLHALGQGHCASLISPWLVSAAHCYIDDRGFRY 666
 + + +R+VGGT + EGEWPWQ SL G+ HICG +LI+ W+++AAHC+ +D
 Sbjct: 559 QGLS--SRIVGGTVSSEGEWPWQASLQIRGR-HICGGALIADRWVITAHCQFQEDS---M 612
 Query: 667 SDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFNDFTFDYDIALLELEKPAEYSSM 726
 + P WT FLG Q+ R PG ++ R+ HP+ + + DYD+ALL+L+ P YS+
 Sbjct: 613 ASPKLWTVFLGKMRQNSRW-PGEVSFKVSRLFLHPYHEEDSHDYDVALQLDHPVVYSAT 671
 Query: 727 VRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTTCENLLPQQITP 786
 VRP+CLP SH F G+ W+TGWG + GG + LQK +++++ Q C Q++P
 Sbjct: 672 VRPVCLPARSHFFEPGQHCWITGWGAQREGGPPVSNLQKVDVQLVPQDLCSEAYRYQVSP 731
 Query: 787 RMMC VGFLSGGVDSCQGDSSGGPLSSVEADGRIFQAGVVSWSGDGCAQRNKPVG YTRLPLFR 846
 RM+C G+ G D+CQGDSSGGPL E GR F AG+VSWG GC + N GYVTR+
 Sbjct: 732 RMLCAGYRKGGKDACQGDSSGGPLVCREPSGRWFLAGLVSWGLGCRPNFFGVYTRVTRVI 791
 Query: 847 DWIKE 851
 +WI++
 Sbjct: 792 NWIQQ 796

☐ >gi|31980537|qb|AAP69827.1|  matriptase-2 [Mus musculus]

gi|37515264|qb|AAH29645.2|  Type II transmembrane serine protease 6 [Mus musculus]
 gi|37089748|sp|Q9DBI0|TMS6 MOUSE Transmembrane protease, serine 6 (Matriptase-2)
 Length = 811

Score = 397 bits (1020), Expect = e-109

Identities = 247/785 (31%), Positives = 378/785 (48%), Gaps = 75/785 (9%)

Query: 83 DVRVQKVFNQGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKESA 142
 +V V +V++G +R+ N +F S F S ++K + L+ L + LG Y+ S+
 Sbjct: 83 EVTVSQVYSGSLRVLNRHFSQDLGRRESIAFRSESAKAQKMLQELVASTR-LGTYYNSSS 141

Query: 143 VTAFSEGSVIAYYWSEFSIPQHLXXXXXXXXXXXXXXXXXXLPPRARSLKSFVVTSVVAFPTD 202
 V +F EG + ++W IP++ L S S + + + D

Sbjct: 142 VYSFGEGPLTCFFWFILDIPEY---QRLTLSPEVVRELLVDELLSNSSTLASYSKTEYEVD 198

Query: 203 SK--TVQRTQDNSCSFGLHARGVELMRFTTPG--FP-DSPYPAHARCQWALRGDADSVLS 257
 + + N G + PG P P C W L+G D ++

Sbjct: 199 PEGLVILEASVNDIVVLNSTLGCYRYSYVNPQGVLPLKGPDQQTTSCLWHLQGPEDLMIK 258

Query: 258 LTFRSFDLASCDERGSIDLTVYNTLSPMEPHALVQLCGTYPPSYNLTFHSSQNVLLITLI 317
 + + C +R V +Y+ P+E + + G + +S +V+ +

Sbjct: 259 VRLE-WTRVDCRDR---VAMYDAAGPLEKRLITSVYGCSRQEPVMEVLASGSVMVAVWK 313

Query: 318 TNTERRHPGF---EATFFQLPRMS-SCGGRLRKAQGTFNSPYYPGHYPPNIDCTWNIEV 372
 + F ++ FQ +++ + GRL QG +PYYP +Y P+ C+W++ V

Sbjct: 314 KGMHSYYDPFLLSVKSVAFQDCQVNLTLLEGRL-DTQGFRLTPYYPSPYSPSTHCSWHLTV 372

Query: 373 PNNQHVKVRKFFYLLEPGVPAGTCPKDYVEINGEKYCGERS-----QFVVTSNSNKITV 427
 P+ + + Y L C + I + CG R+ + + S+ +T+

Sbjct: 373 PSLDYGLALWFDAYALRRQKYNRLCTQGQWMIQNRRLCGFRTLQPYAERIPMVASDGVTI 432

Query: 428 RFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRGTGR CIRKELRCDGWADCTDHSDELNCS 487
 F S S T G Y Y+ SDPCPG+F C

Sbjct: 433 NFTSQISLTGPGVQVYYSLYNQSDPCPGEF LCSV----- 466

Query: 488 CDAGHQFTCKNKFKPLFWVCDSDVDCGNSDEQGCSCPAQTFRCs-NGKCLSKSQQCNG 546
 N C P CD + DC + DE+ C C A F+C + C+S + C+

Sbjct: 467 -----NGLCVP---ACDGIKDCPNGLDERNCVCRAM-FQCQEDSTCISLPRVCDR 512

Query: 547 KDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGL 606
 + DC +GSDE C + V C T++C + C+ K NPECDG+ DC DGSDE+ CDCGL

Sbjct: 513 QPDCLNGSDEEQCEG--VPCGTFTFQCEDRSCVKPNPECDGQSDCRDGSDEQHCDCGL 570

Query: 607 RSFTRQARVVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRY 666
 + + +R+VGGT + EGEWPWQ SL G+ HICG +LI+ W+++AAHC+ +D

Sbjct: 571 QGLS--SRIVGGTVSSEGEWPWQASLQIRGR-HICGALIADRWVITAACHCFQEDS---M 624

Query: 667 SDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSM 726
 + P WT FLG Q+ R PG ++ R+ HP+ + + DYD+ALL+L+ P YS+

Sbjct: 625 ASPKLWTVFLGKMRQNSRW-PGEVSFKVSRLFLHPYHEEDSHDYDVALQLDHPVVYSAT 683

Query: 727 VRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQQITP 786
 VRP+CLP SH F G+ W+TGWG + GG + LQK +++++ Q C Q++P

Sbjct: 684 VRPVCLPARSHFFEPGQHCWITGWGAQREGGPVSNTLQKVDVQLVPQDLCSEAYRYQVSP 743

Query: 787 RMMCVGFLSGGVDSCQGDSSGGPLSSVEADGRIFQAGVVSWSGDGCAQRNKP GYVTRLPLFR 846
 RM+C G+ G D+CQGDSSGGPL E GR F AG+VSWG GC + N GYVTR+

Sbjct: 744 RMLCAGYRKGGKDACQGDSSGGPLVCREPSGRWFLAGLVSWGLGCGRPNFFGVYTRVTRVI 803

Query: 847 DWIKE 851
 +WI++

Sbjct: 804 NWIQQ 808

☐ >gi|27229129|ref|NP_082178.1| ☒ type II transmembrane serine protease 6 [Mus mus
 gi|26338412|dbj|BAB23684.2| ☒ unnamed protein product [Mus musculus]
 Length = 812

Score = 395 bits (1014), Expect = e-108
 Identities = 248/786 (31%), Positives = 379/786 (48%), Gaps = 76/786 (9%)

Query: 83 DVRVQKVFNGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPHYKESA 142
 +V V +V++G +R+ N +F S F S ++K + L+ L + LG Y+ S+
 Sbjct: 83 EVTVSQVYSGSLRVLNHRHFSQDLGRRESIAFRSESAKAQKMLQELVASTR-LGTYYNSSS 141

Query: 143 VTAFSEGSVIAIYWSEFSIPQHLXXXXXXXXXXXXXXXXLPPRARSLKSFVVTSVVAFPTD 202
 V +F EG + ++W IP++ L S S + + + D
 Sbjct: 142 VYSFGEGLTCCFFWFILDIPEY---QRLTSLPEVVRELLVDELLSNSSTLASYSKTEYEVD 198

Query: 203 SK--TVQRTQDNCSFGLHARGVELMRFTTPG--FP-DSPPAHARCQWALRGDADSVLS 257
 + + N G + PG P P C W L+G D ++
 Sbjct: 199 PEGLVILEASVNDIVVLNSTLGCYRYSYVNPQVPLPKGPDQQTTSCLWHLQGPEDLMIK 258

Query: 258 LTFRSFDLASCDEGSDLVTVYNTLSPEPHALVQLCGTYPPSYNLTFFHSSQNVLLITLI 317
 + + C +R V +Y+ P+E + + G + +S +V+ +
 Sbjct: 259 VRLE-WTRVDCRDR----VAMYDAAGPLEKRLITSVYGCSRQEPVMEVLASGSVMVAVWK 313

Query: 318 TNTERRHPGF----EATFFQLPRMS-SCGGRLRKAQGTFNSPYYPGHYPNIDCTWNIEV 372
 + F ++ FQ +++ + GRL QG +PYYP +Y P+ C+W++ V
 Sbjct: 314 KGMHSYYDPFLLSVKSVAFQDCQVNLTLLEGRL-DTQGFLRTPYYPSYSPSTHCSWHLTV 372

Query: 373 PNNQHVQVRFKFFYLLEPGVPAGTCKDYVEINGEKYCGERS-----QFVVTNSNKNITV 427
 P+ + + Y L C + I + CG R+ + + S+ +T+
 Sbjct: 373 PSLDYGLALWFDAYALRRQKYNRLCTQGQWMIQNRRLCGFRTLQPYAERI PMVASDGVTI 432

Query: 428 RFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCTDHSDELNCS 487
 F S S T G Y Y+ SDPCPG+F C
 Sbjct: 433 NFTSQISLTGPGVQVYYSLYNQSDPCPGEFLCSV----- 466

Query: 488 CDAGHQFTCKNKFKPLFWVCDVNDGDNDEQGCSCPAQTFRCS-NGKCLSKSQQCNG 546
 N C P CD + DC + DE+ C C A F+C + C+S + C+
 Sbjct: 467 -----NGLCVP---ACDGIKDCPNGLDERNCVCRAM-FQCQEDSTCISLPRVCDR 512

Query: 547 KDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGSDEKDCDCGL 606
 + DC +GSDE C + V C T++C + C+ K NPECDG+ DC DGSDE+ CDCGL
 Sbjct: 513 QPDCLNGSDEEQCEG--VPCGTFTFQCEDRSCVKKPNPECDGQSDCRDGSDEQHCDCGL 570

Query: 607 RSFTRQARVVGTTDADEGEWPWQVSLHALGQGHICGASLISPWLVSAAHCYIDDRGFY 666
 + + +R+VGGT + EGEWPWQ SL G+ HICG +LI+ W+++AAHC+ +D
 Sbjct: 571 QGLS--SRIVGGTVSSEGEWPWQASLQIRGR-HICGALIADRWVITAACHCFQEDS---M 624

Query: 667 SDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFNDFTFDYDIALLELEKPAEYSSM 726
 + P WT FLG Q+ R PG ++ R+ HP+ + + DYD+ALL+L+ P YS+
 Sbjct: 625 ASPKLWTVFLGKMRQNSRW-PGEVSFKVSRLFLHPYHEEDSHDYDVALQLDHPVVYSAT 683

Query: 727 VRPICLPDA-SHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTNENLLPQQIT 785
 VRP+CLP A SH F G+ W+TGWG + GG + LQK +++++ Q C Q++
 Sbjct: 684 VRPVCLPPARSHFFEPGQHCWITGWGAQREGGPVSNTLQKVDVQLVPQDLCSEAYRYQVS 743

Query: 786 PRMMCVGFLSGGVDSCQGDSSGGLSSVEADGRIFQAGVVSWDGCAQRNKPVGYYTRLPLF 845
 PRM+C G+ G D+CQGDSSGGL E GR F AG+VSWG GC + N GYVTR+
 Sbjct: 744 PRMLCAGYRKGGKDACQGDSSGGLVCREPSGRWFLAGLVSWGLGCGRPNFFGVYTRVTRV 803

Query: 846 RDWIK 851
 +WI++
 Sbjct: 804 INWIIQ 809

☐ >gi|23957702|ref|NP_705837.1|  transmembrane protease, serine 6 [Homo sapiens]

gi|23428417|gb|AAL16414.1| **G** type II transmembrane serine protease 6 [Homo sapiens]
gi|23428409|gb|AAL16413.1| **G** type II transmembrane serine protease 6 [Homo sapiens]
gi|37088915|sp|Q8IU80|TMS6 HUMAN **G** Transmembrane protease, serine 6 (Matriptase-2)
Length = 811

Score = 393 bits (1009), Expect = e-107

Identities = 249/794 (31%), Positives = 370/794 (46%), Gaps = 91/794 (11%)

Query: 83 DVRVQKVFNQGYMRITNENFVDAYENSNSTEFVSLASKVKDALKLLYSGVPFLGPYHKESA 142
+V V +V++G +R+ N +F S+ F S +K + LK L + LG Y+ S+
Sbjct: 81 EVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTR-LGTYYNSSS 139

Query: 143 VTAFSEGSVIAIYWSEFSIPQHLXXXXX-----XXXXXXXXXXLPPRARSLKSF 191
V +F EG + ++W IP+H +P RA
Sbjct: 140 VYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY--EV 197

Query: 192 VVTSVVAFPDTSKTVQRTQDN-SCSFGHLHARGVELMRFTTPGFPDSPYPAHARCQWALRG 250
+V K + C + +++R P S C W L+G
Sbjct: 198 DPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLKGPDLHLASS-----CLWHLQG 251

Query: 251 DADSVLSLTFRSDLASCDERGSIDLTVTYNTLSPMEPHALVQLCGTYPSPYNLTFHSSQN 310
D +L L + LA C +R + +Y+ P+E + + G + +S
Sbjct: 252 PKDLMLKLRLE-WTLAECRDR----LAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGA 306

Query: 311 VLLITLITNTERRHPGF----EATFFQLPRMSSCGGRLRKAQGTFNSPYYPGHYPNIDC 366
++ + + F + FQ ++ +QG ++PY+P +Y P C
Sbjct: 307 IMAVVWKKGLHSYYDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLPSTPYFPSYSPQTHC 366

Query: 367 TWNIEVPNNQHVKVRFKFFYLLEPGVPAGTCKPDYVEINGEKYCG-----ERSQFVV 418
+W++ VP+ + + Y L C + I + CG ER V
Sbjct: 367 SWHLTVPSLDYGLALWFDAYALRRQKYDLPCQTQGWTIQNRRLCGLRILQPYAERIPVVA 426

Query: 419 TSNSNKITVRFHSDQSYTDTGFLAEYLSYDSSDPCPGQFTCRTGRCIRKELRCDGWADCT 478
T+ IT+ F S S T G Y Y+ SDPCPG+F C
Sbjct: 427 TAG---ITINFTSQISLTGPGVRVHYGLYNQSDPCPGEFLCSV----- 466

Query: 479 DHSDELNCSCDAGHQFTCKNKFKPLFWVCDSDVNDGSDQGCSCPAQTFRCSS-NGKC 537
N C P CD V DC + DE+ C C A TF+C + C
Sbjct: 467 -----NGLCVP---ACDGVKDCPNGLDERNCVCRA-TFQCKEDSTC 503

Query: 538 LSKSQQCNGKDDCGDGSDEASCPKVNVTCTKHTYRCLNGLCLSKGNPECDGKEDCSDGS 597
+S + C+G+ DC +GSDE C + V C T++C + C+ K NP+CDG+ DC DGS
Sbjct: 504 ISLPKVCQGPDCLNGSDEEQCEG--VPCGTFTFQCEDRSCVKKPNPQCDGRPDGRDGS 561

Query: 598 DEKDCDCGLRSFTRQARVVGTTDADEGEWFPWQVSLHALGQGHICGASLISPNWLVSAAHC 657
DE+ CDCGL+ +R+VGG + EGEWFPWQ SL G+ HICG +LI+ W+++AAHC
Sbjct: 562 DEEHDCDGLQG--PSSRIVGGAVSSEGEWFPWQASLQVRGR-HICGGALIADRWVITAHC 618

Query: 658 YIDDRGFRYSPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLEL 717
+ +D + WT FLG Q+ R PG ++ R++ HP+ + + DYD+ALL+L
Sbjct: 619 FQEDS---MASTVLWTVFLGKVVQNSRW-PGEVSFKVSRLLLHPYHEEDSHDYDVALQL 674

Query: 718 EKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCE 777
+ P S+ VRP+CLP SH F G W+TGWG + GG + LQK ++++I Q C
Sbjct: 675 DHPVVRSAAVRPVCLPARSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCS 734

Query: 778 NLLPQQITPRMCMVGLSGGVDSCQGDSSGGLSSVEADGRIFQAGVVSWDGCAQRNKP 837
+ Q+TPRM+C G+ G D+CQGDSSGGL GR F AG+VSWG GC + N G
Sbjct: 735 EVYRYQVTPRMLCAGYRKGGKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCGRPNYFG 794